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Result
No.
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                 Score
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length: 2000000000
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Query
Match
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Gapop 10.0 ,
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/genesed/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

4: /SIDS1/gcgdata/genesed/geneseqp-emb1/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

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1063
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                                                                                                                                                                                                                                                                                    /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT: *
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT: *
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  IJ
AAY73837
AAY76590
AAG75621
AAW77365
AAW37844
AAW37872
AAB24070
AAU08804
AAB72203
AAB72203
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(without alignments)
715.038 Million cell updates/sec
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          Human prostate tum
Human ovarian tumo
Human colon cancer
zsig10 polypeptide
Human xAc growth f
Human protein comp
secreted protein 1
Human PRO1030 prot
Breast cancer cell
Human huXAG-1/CCSG
                                                                                                                                                              Description
 Human secreted pro
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AAY73837
ID AAY7
  PSXTTTX
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                                                                                                                                                                                                                                                                                                                                                                                                   AAY73837;
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ALIGNMENTS

(first entry)

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WPI; 199
N-PSDB;
Claim 23; Page 318; 502pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                   treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Pancreas; tumor; EST; expressed sequence tag; human; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human prostate tumor EST fragment derived protein #24
                                       proteins
                                             New human nucleic acid sequences from pancreatic tumors, and related proteins
                                                                                                                                                 Rosenthal A, Specht T,
                                                                                                                                                                                        (META-) METAGEN GES GENOMFORSCHUNG MBH
                                                                                                                                                                                                                             28-APR-1998;
                                                                                                                                                                                                                                                                28-APR-1998;
                                                                                                                                                                                                                                                                                                      04-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                            1999-621386/54.
DB; AAZ52865.
                                                                                                                                                                                                                             98DE-1020190
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                                                                                                                                                   Hinzmann B,
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Best Local Similarity
This invention describes novel nucleic acid (cDNA) sequences (A) which have anticancer activity and are highly expressed in ovarian tumor tissue (and some also in testis and breast cancer tissue). The products of the invention can be used for gene therapy. (A) are used (i) for recombinant expression of polypeptides (B) and (ii) to isolate complete
                                                                                                                                                                      WPI; 1999-591920/51.
N-PSDB; AAZ77486.
                                                                                    Claim 25; Page 279; 310pp; German.
                                                                                                             New nucleic acid sequences expressed tissues, and derived polypeptides, for identification of therapeutic agents
                                                                                                                                                                                                                                                                                                  09-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel polypeptides and their encoding nucleic acids derived from human pancreatic tumor tissue which have cytostatic activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. ANY73814-Y74252 represent protein fragments encoded by the human pancreatic tumor cDNA library derived expressed sequence tag (EST) sequences represented in
                                                                                                                                                                                                                Rosenthal A,
                                                                                                                                                                                                                                          (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                                                                                                                                                                                                                                       09-APR-1998;
                                                                                                                                                                                                                                                                                                                                                         DE19817557-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represent protein fragments encoded by library derived expressed sequence tag AAZ52858-Z53014.
                                                                                                                                                                                                                                                                                                                             21-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                           Expressed sequence tag; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY76590 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKDTKDSRPKLPQTLSRGWGDQLIWTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLSCAGTLSGSGPHPSRRLTQGRWVRKSRVAMEKIPVSAFLLLVALSYTLARDTTVKPGA 60
                                                                                                                                                                                                                                                                                                                                                                                                             therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YAYEPADTALLLDNMKKALKLLKTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VFAENKEIQKLAEQFVLLNLVYETTDKHLSPDGQYVPRIMFVDPSLTVRADITGRYSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLSCAGTLSGSGPHPSRRLTQGRWVRKSRVAMEKIPVSAFLLLVALSYTLARDTTVKPGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKDTKDSRPKLPQTLSRGWGDQLIWTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumor EST fragment encoded protein
                                                                                                                                                                                                                Specht T,
                                                                                                                                                                                                                                                                                                                                                                                                               treatment
                                                                                                                                                                                                                                                                      98DE-1017557.
                                                                                                                                                                                                                                                                                                  98DE-1017557.
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                                                                                                                                                                                                                Hinzmann
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                                                                                                                                                                                                                                                                                                                                                                                                                           human; ovarian tumor; anticancer;
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Pred. No. 2.3e-108;
; Mismatches 0;
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treatment
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of c
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                                                                                                                             d some other, cancer ovarian cancer and
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RESULT 3
AAG75621
ID AAG7
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Best Local S
Matches 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genes. (B) are used (1) to identify agents suitable for treatment of ovarian cancer; (ii) directly for treating this form of cancer (including expression from gene therapy vectors) and (ii) for generation of specific antibodies. (A) are identified by assembling ESTs (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTs from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. AAV76505-Y76638 represent protein fragments encoded by the human ovarian tumor cDNA library derived EST fragments represented in AAZ77450-Z77572.
                                                             Nucleic
                                                                                                                                                                           29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                               28-SEP-2000; 2000WO-US26524
                                                                                                                                                                                                                                         05-APR-2001.
                                                                                                                                                                                                                                                                 WO200122920-A2
                                                                                                                                                                                                                                                                                                                   colorectal carcinoma
                                                                                                                                                                                                                                                                                                                               Human; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                 03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                AAG75621 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                        Human colon
                                                                                                                                                                                                                                                                                                                                                                                                        AAG75621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
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                                                                                     2001-235357/24.
)B; AAH35026.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNMKKALKLLKTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QTLSRGWGDQLIWTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QTLSRGWGDQLIWTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHPSRRLTQGRWVRKSRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNMKKALKLLKTEL
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                                                                                                                          SM,
                                               acids encoding for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                       Page 7865-7866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194
                                                                                                                          Barash
                                                                                                                                                                                                                                                                                                                                                      cancer antigen
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                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                            99US-0157137.
99US-0163280.
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                                                                                                                                                                                                                                                                                                                               colon
                                              4277 human
diagnosing
                                                                                                                          Birse
                      9803pp;
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                                                                                                                           CE,
                      English
                                                and/or treating
                                                             colon cancer-associated
                                                                                                                           Rosen
                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO:6385
                                                                                                                                                                                                                                                                                                                             diagnosis;
                                                colorectal cancers -
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                                                                                                                                                                                                                                                                                                                                detection;
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AAH32943 to AAH37195

and

AAG73514

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AAG77788

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RESULT 4
AAW77365
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N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P
                                                                                                                                                                                                                                                                                                                                                                                                                            Human; mucous-mediated function; adhesion; tumour metastasis; bacterial colonisation; microbial infection; AIDS; cystic fibrosis; chronic obstructive pulmonary disease; asthma; Crohn's disease; sinonasal inflammatory disease; inflammatory bowel disease; bronchi
                     WPI; 1998-531566/45
                                                                    Sheppard
                                                                                                                                                                                                                                                                            24-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        zsig10 polypeptide
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N-PSDB; AAV59320.
                                                                                                                                                                          19-MAR-1997;
                                                                                                                                                                                                                            18-MAR-1998;
                                                                                                                                                                                                                                                                                                                           W09841627-A1
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-DEC-1998
                                                                                                                           ( ZYMO )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 PHPSRRLTQGRWVRKSRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QTLSRGWGDQLIWTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHPSRRLTQGRWVRKSRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLP
                                                                                                                        ZYMOGENETICS
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                                                                         РО
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                          97US-0039631
                                                                                                                                                                                                                            98WO-US05251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.3%;
100.0%;
                                                                                                                           INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1002; DB 22;
Pred. No. 1.1e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                               inflammatory bowel disease; bronchitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89
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                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The human polypeptide zsig10 is involved in mucous-mediated functions such as adhesion. The products of the invention can be used in the stu and treatment of e.g. tumour metastasis, bacterial colonisation, susceptibility to and persistence of infection, microbial infections, AIDS, cystic fibrosis, chronic obstructive pulmonary disease, asthma, sinonasal inflammatory disease, inflammatory bowel disease, bronchitis, or Crohn's disease. The products can also be used for detection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated mucous-associated polypeptide, zsig10 - used to developroducts for treating e.g. tumour metastasis, microbial infections, cystic fibrosis, asthma, bronchitis or inflammatory bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                         AAW37844 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                wound healing; diagnosis; therapy; human.
                                                                                                                                                                                                                                                                                                                                     Human XAG growth factor huXAG-1.
                                Peptide
                                                                    Peptide
                                                                                                    Peptide
                                                                                                                                      Peptide
                                                                                                                                                                       Peptide
                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                HuXAG-1;
                                                                                                                                                                                                                                                                                                                                                              28-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                XAG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                   growth factor; colon cancer; tumour marker;
e; liver disease; lung disease; emphysema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          drug
/label= Epitope
/note= "Claim 12"
138..150
                                  /note= "Claim
113..125
                                                                                                                           /label=
                                                                                                                                                             /label=
                                                                                                                                                                                                                                            Location/Qualifiers
                                                        /label=
                                                                             /note=
                                                                                           'label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           screening.
                                                                                                                                                                                                                                                                                                                                                                                                          Protein; 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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                                                                                                                                                 = Epitope
Claim 12"
                                                                                                                                                                                  "Mat_protein
"Claim 11"
                                           Epitope "Claim 12"
                                                                             Epitope
"Claim 12"
                                                                               "Claim
                                                                                                                "Claim
                                                                                                                           Epitope
                                                                                                                                                                                                                    Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 899; DB 19;
Pred. No. 1.8e-90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 175;
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                                                                                                                                                                                                                                                                                                                                              chuman growth factors also including huxag-2 (see AAW37845) and the huxag-3 (see AAW37846). These proteins share homology with the CC XAG protein of Xenopus laevis, which is involved in embryogenesis CC and is expressed in adult tissue. huxag-1 is specifically found CC in cancer. huxag-1 cDNA (see AAV1915) was isolated from a cDNA CC library derived from human colon cancer tissue. Vectors, host CC colon cancer. huxag-1 cDNA (see AAV1915) was isolated from a cDNA CC library derived from human colon cancer tissue. Vectors, host CC colls, antibodies, and screening methods for identifying agonists CC colls, antibodies, and screening methods for identifying agonists CC colls, antibodies, and screening methods for identifying agonists CC colls, antibodies, and screening methods for identifying agonists CC colls, antibodies, and screening methods for identifying agonists CC colls, antibodies, and screening methods for identifying agonists CC colls, antibodies, and screening methods for identifying agonists CC colls, antibodies, and screening methods for identifying agonists CC colls, antibodies, and screening methods for identifying agonists CC colls, antibodies, and screening methods for identifying agonists colleges colls, antibodies, and screening methods for identifying agonists colleges colleges colleges colleges and toxic substances. They can also be used to stimulate proliferation and differentiation and promote the repair CC colls, and bronchiolar pathological states. They can be used to stimulate proliferation and differentiation and promote the repair colleges colleges of alveoli, and inhalation injuries, e.g. cresulting from smoke inhalation and burns, that cause necrosis of the bronchiolar epithelium and alveoli. They can also be used to stimulate the proliferation and differentiation of breast tissue and could therefore be used to promote healing of breast tissue used columb to the colleges of t
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                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                              injury due to surgery, trauma or cancer. Antagonists can be to treat hyperproliferative disorders, including cancer, in particular hepatocellular carcinoma, osteoclastoma, breast cor colon cancer. The products can also be used for detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 1; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated human XAG growth factor(s) - used to develop products for treating e.g. liver, lung or breast diseases or hyperproliferative disorders, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-169093/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-AUG-1997;
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  121
                                          152
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                                                                                                                                                                 Local Similarity
                 DGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL 206
  DGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL
                                                                                                        ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
                                                                                    ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
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                                                                                                                                                                                                                                                                                                                                              175
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                                                                                                                                                                                                                                                          Conservative
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/note= "Claim 12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprises huxAG-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prises huXAG-1, a member of a novel family also including huXAG-2 (see AAW37845) and
                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endress
                                                                                                                                                                                                                                                       Score 899; DB 19;
; Pred. No. 1.8e-90;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GA,
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د
                                                                                                                                                                                                                                                                                               Length 175;
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                          detection
                                                                                                                                                                                                                                                                                                                                                                                                                           breast cancer,
                                                                                                                                                                                                                                                       0;
175
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RESULT 7
AAY59675
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AAW37872
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                                                                                                                                                                                                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                                               This is the amino acid sequence of a novel human protein comprising a secretory signal isolated from stomach cancer cells. Its proteins can be used as nutritional sources or supplements. The proteins may also have cytokine functions, immune modulating functions, haematopoiesis regulating activity, activiny/inhibin regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPT; 1998-207380/18.
N-PSDB; AAV29047, AAV29048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human protein; secretory signal; nutritional source; immunity; haematopolesis; activin; inhibin; tumour; cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW37872 standard; Protein;
                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Pages 79; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 disorders, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                               Human proteins with secretory signal sequences - used to tre-
immune deficiencies, infections, tumours, and haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PROT-) PROTEGENE INC. (SAGA) SAGAMI CHEM RES CENTRE.
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                                                                                                                                                                                                                                                                                                                                                                                                                             immune deficiencies,
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                                                           MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE
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                                                                                                                       ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
                                                                                                                                                             MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE
                                                                                                            ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                            175
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                            ΑĄ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-JP03239
                                                                                                                                                                                                           84.6%; Score 899; DB 19;
100.0%; Pred. No. 1.8e-90;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sekine S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence
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                                                                                                                                                                                                             Gaps
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AAY59675 standard; Protein; 175

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Query Match
Best Local Sin
Matches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                          tissue types or cell species, as well as identifying tissue specific soluble proteins. The sequences can be used for chromosome mapping and identification of genes associated with hereditary diseases or drug response. Signal sequences from the cDNAs can be used in construction of secretion vectors. Other sequences derived from the extended cDNAs can be used to clone upstream genomic DNA sequences including promoters. This is in turn useful for identifying proteins that interact with promoter sequences. Some of the proteins may be useful in diagnosing and treating several disorders including, but not limited to: cancer, hyperlipidaemia, cardiovascular and neurodegenerative disorders, autoimmune diseases, and rheumatic diseases, embryogenic disorders, hypertension, renal injury, amino acidurias, hypoglycaemia, male rat infertility and myopathies.
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13-APR-1998;
10-AUG-1998;
04-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a human secreted protein of the invention. The extended cDNAs (or genomic DNAs obtainable from them) may be used to prepare PCR primers and probes. These are useful for forensic matching or positive identification by DNA sequencing. They may also be used in alternative fingerprint identification techniques. Antibodies against the proteins encoded by the extended cDNAs are useful in identification of the protein second by the extended cDNAs are useful in identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Extended
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secreted
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     152
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DGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL 206
                                                                                 ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
                                                                                                                                                                                            MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE
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                                                                                                                                                          MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE
                                                     ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Page 199; 244pp; English.
                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNAs useful
antibodies -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; fingerprint identification technique,
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                                                                                                                                                                                                                                                                           Conservative
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98US-0081563.
98US-0096116.
98US-0099273.
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                                                                                                                                                                                                                                                                     Score 899; DB 20;
Pred. No. 1.8e-90;
0; Mismatches 0;
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ID AAB2
26-JUL-1999;
30-NOV-1999;
20-DEC-1999;
05-JAN-2000;
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02-JUN-1999;
23-JUN-1999;
07-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; tumour; diagnosis; neoplastic disease; neoplastic cell growt proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive; immunostimulant; antianglogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; anglogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                          14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammatory disorder; immunologic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-2001
                                                                                                                                                                                                                                                                                                   GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                        2000WO-US00376
                                                                                                                                                                                                                                                                                                                                                         99WO-US12252.
99US-0141037.
99US-0143048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis; neoplastic disease; neoplastic cell growth;
tumourigenesis; identification; cancer; cytostatic;
                                                                                                                                                                                                                                                                                                                                       99US-0145698
99WO-US28313
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Thirty PRO polynucleotides encoding treatment, diagnosis and prevention of cancer PRO polypeptides, useful in

N-PSDB; AAC58380

2000-572270/53

Watanabe CK, Ashkenazi AJ,

Wood

WI;

Baker KP,

Goddard A,

Gurney AL,

Hillan KJ,

Roy MA;

Claim 61; Fig 28; 286pp; English.

CC one of the human PRO proteins designated PRO211, PRO290, PRO341, PRO335, CC PRO519, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, CC PRO5197, PRO1030, PRO1097, PRO11107, PRO11117, PRO11182, PRO1009, CC PRO1187, PRO1281, PRO233, PRO339, PRO834, PRO1317, PRO1170, PRO2094, CC PRO1187, PRO12881, PRO233, PRO339, PRO834, PRO1317, PRO11710, PRO2094, CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell CC growth. The PRO polypeptides and nucleotides are useful in the CC treatment, diagnosis and prevention of cancer. The antibodies and other CC anti-tumour compounds maybe used to treat various conditions, including those characterised by overexpression and/or activation of the amplified CC progress. Exemplary conditions or disorders to be treated with such CC antibodies and other compounds include benign or malignant tumours CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours), CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours), CC epithelial, stromal and blastocoelic disorders, and inflammatory, CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR primers and hybridisation probes used in the isolation of the human PRO The present invention describes an isolated antibody that binds

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
The invention describes the novel use of a protein found in breast cancer cell membranes (BCMP 7) for diagnosing, preventing and treating breast cancers. The peptide has cytostatic action and potential uses in gene therapy and in vaccines. The polypeptide, antisense nucleic acids, or fusion proteins comprising and Green Fluorescent protein or the DsRR Fluorescent protein, antibodies specific for and/or nucleic acid are used for the prevention and/or treatment of breast cancer. Antibodies against may also be used for screening for and/or diagnosis of breast
                                                                                                                                      Diagnosing, cell membra
                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Breast cancer cell membrane protein 7; BCMP 7; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Breast cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU08804 standard;
                                                                                                                                                                                                                                                             25-FEB-2000; 2000GB-0004576
                                                                                                                                                                                                                                                                                     21-FEB-2001; 2001WO-GB00734.
                                                                                                                                                                                                                                                                                                                                                                          Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human polynucleotide and protein sequences given in the exemplification of present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE 91
                                                                                                                                      nosing, preventing and membrane protein BCMP
                                                                                                                                                                                      2001-570651/64.
                                                                                                                                                                                                               RS,
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                                                                                                            62pp;
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21..175
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                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine
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                                                                                                               English.
                                                                                                                                                                                                               Terrett JA,
                                                                                                                                                                                                                                                                                                                                                             "Mature BCMP 7"
                                                                                                                                          treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy; antibody; antisense;
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                                                                                                                                                                                                               Tyson KL;
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1.8e-90;
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                                                                                                                                                     breast cancer
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AAB72203
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Query Match
Best Local
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        This invention relates to a human growth factor polypeptide huXAG-1 also known as a colon cancer specific gene (CCSG). HuXAG-1 stimulates cell proliferation as a growth factor. The HuXAG-1 protein is useful for identifying compounds capable of enhancing or inhibiting cellular response induced by huXAG-1. The protein is also useful for stimulating proliferation of cells e.g. colon, breast, liver and lung cells, and hepatocytes. It is useful for alleviating or treating liver diseases and pathologies such as fulminant liver failure caused by cirrhosis, liver damage caused by viral hepatitis and toxic substances, for preventing and treating damage to the lungs caused by various pathological states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; growth factor; huxAG-1; colon cancer specific gene; (cell proliferation; liver disease; fulminant liver failure; hepatitis; cancer; colon cancer; colorectal carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB72203 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB72203;
                                                                                                                                                                       Claim 165; Fig 1; 59pp; English.
                                                                                                                                                                                                  Novel human growth factor polypeptide useful for diagnosing and treating colon cancer and liver diseases, to prevent and heal dithe lungs and for identifying modulators of therapeutic use -
                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                     Ľ
                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                          23-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                        22-AUG-1997;
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                                                                                                                                                                                                                                                                         2001-136872/14.
                                                                                                                                                                                                                                                                                                     Dillon PJ,
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RESULT 11
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      Query Match
Best Local S
Matches 175
The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer. HuXAG-1 and the identified antagonist are useful for treating cancer, in particular colon cancer. Detecting altered levels of huXAG-1 and its polynucleotides are useful for diagnosing or detecting cancer in mammals. The gene encoding huXAG-1 is useful for monitoring human colorectal carcinoma. huXAG-1 nucleic acid molecules are also useful for
                                                                                                                                                                                                             New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond
                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                     Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted
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                                                                                                                                                                      Claim 13;
                                                                                                                                                                                                  diagnostic, forensic,
                                                                                                                                                                                                                                                                                                                                                                 26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                              21-FEB-2000;
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llarity 100.0%;
Conservative (
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                                                                                                                                                                    ID 4190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome mapping.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expressed sequence
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                                                                                                                                                                                                                                                                                                                                                                 99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                               gene therapy and chromosome mapping
                                                                                                                                                                    71pp + CD-ROM;
                                                                                                                                                                                                                                                                                                     Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tag; secreted protein; cDNA isolation;
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                                                                                                                                                                                                                                                                                                       Giordano
                                                                                                                                                                    English.
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1.8e-90;
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Best Local :
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                                                                                                                                                                                                                                                                            09-FEB-1998;
13-APR-1998;
10-AUG-1998;
04-SEP-1998;
                                                                                                                                             Extended specific
                                                                                                                                                                                  WPI; 199
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secreted protein; fingerprint identification tecnnique; cancer; chromosome mapping; human; hereditary disease; diagnosis; cancer; hyperlipidaemia; cardiovascular; neurodegenerative disorder; therapy; autoimmune disease; rheumatic disease; embryogenic disorder; myopathy; renal injury; amino aciduria; hypoglycaemia; male rat infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
The extended cDNAs (or genomic DNAs obtainable from them) may be used to prepare PCR primers and probes. These are useful for forensic matching or positive identification by DNA sequencing. They may also be used in alternative fingerprint identification techniques. Antibodies against the proteins encoded by the extended cDNAs are useful in identification of tissue types or cell species, as well as identifying tissue specific soluble proteins. The sequences can be used for chromosome mapping and
                                                                                                                     Claim 10;
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                                                                                           This sequence represents a human secreted protein of the invention.
                                                                                                                                                                                                                         Bougueleret L,
                                                                                                                                                                                                                                                                                                                                            09-FEB-1999;
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DB; AAZ40846.
                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens.
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                                                                                                                                             cDNAs useful antibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                   Page 240; 244pp; English.
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                                                                                                                                                                                                                                                                            98US-0074121.
98US-0081563.
98US-0096116.
98US-0099273.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
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Pred. No. 5.9e-64;
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                                                                                                                                                           proteins and
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RESULT 13
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Best Local
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AAX41094 to AAX41347 represent 5' expressed sequence tags (ESTs) for human secreted proteins, and encode the proteins given in AAX12261 AAX12514, respectively. The proteins given represent the signal pep
                                                                                              New nucleic acids encoding human secreted proteins - objection of the color libraries prepared from e.g. liver, ovary, brain, platenty, lung, umbilical cord, placenta and colon tissue
                                                                  Claim 27;
                                                                                                                                                                                                        Duclert A,
                                                                                                                                                                                                                                                                     01-AUG-1997;
                                                                                                                                                                                                                                                                                                  31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                11-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                      differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     forensic; gene therapy; chromosome mapping; signal peptide;
upstream regulatory sequence; cytokine activity; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human 5′
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY12312 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                     (GEST )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dentification of genes associated with hereditary diseases or drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 XLXKSKTSNKPLMIIHHLDXCPHSQALKKXFAENKXIQKLAXQFVXLNLVYETTDKHLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 117; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1
                                                                                                                                                                          1999-153778/13
                                                                                                                                                                                                                                                                                                                                                                                           sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGQYXP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEKIPVSAFLLIVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGQYVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              secreted protein; EST; expressed sequence tag; diagnosis;
                                                                                                                                                                                                                                       GENSET
                                                                                                                                                             AAX41145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST secreted protein SEQ ID NO:343
                                                                  Page 682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131
                                                                                                                                                                                                        Dumas Milne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        anti-inflammatory; tumour inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                       97US-0905135
                                                                                                                                                                                                                                                                                                  98WO-IB01222
                                                               824pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.9%;
                                                                                                                                                                                                        Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116
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Pred. No. 2.3e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                        Lacroix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 131;
                                                                                                                              obtained
    signal peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, receptor/ ligand activity, anti-inflammatory activity, receptor/ ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for polypeptide into a membrane, or importing a polypeptide into a cell.
AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST) sequences, corresponding to human secreted proteins. AAY64651 to AAY64438 represent the EST-related proteins corresponding to AAZ42265 AAZ43053. The 5' ESTs can be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated
                                                                                                                                                                                                                                                 09-APR-1998;
28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy; chromosome mapping; upstream regulatory sequence;
                                                                                                            diagnostic,
                                                                                                                                                                WPI; 2000-038446/03
                                                                                                                                                                                                                                                                                        09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human 5' EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY64672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY64672 standard; Protein;
                                                                                                                      Novel secreted protein 5' expressed
                                                                                                                                                                                                                      (GEST
                                                                                                                                                                                                                                                                                                                   21-OCT-1999.
                                                                                                                                                                                                                                                                                                                                            WO9953051-A2
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                regulation; identification.
                                                                                                                                                                                                                                                                                                                                                                                                              forensic; location; development;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al Similarity
116; Conserv
                                                                                                                                                                                           Milne
                                                                                                                                                                                                                                                                                                                                                                                                                                        5' EST;
                                                                                Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 AA;
                                                                                                            forensic,
                                                                                                                                                                                           Edwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                604; 837pp;
                                                                                                                                                                                                                                               98US-0057719
98US-0069047
                                                                                                                                                                                                                                                                                       99WO-IB00712
                                                                                                                                                                                                                                                                                                                                                                                                                                        expressed sequence tag; secreted protein; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide SEQ ID NO:833
                                                                                                            gene
                                                                                                                                                                                           Duclert
                                                                                 English.
                                                                                                           therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                           sequence tag sequences used and chromosome mapping proce
                                                                                                                                                                                            Giordano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.2e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20;
                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 116;
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                                                                                                                                                                                                                                                                                                                                                                                                                stability;
                                                                                                            procedures
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RESULT 15
AAW37846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
WPI; 1998-169093/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW37846 standard; Protein; 166 AA
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                                                                                                                                                                                                                                                                                  W09807749-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-AUG-1998 (first entry)
                                              Dillon PJ,
                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                           23-AUG-1996;
                                                                                                                                                                                        22-AUG-1997;
                                                                                                                                                                                                                                      26-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HuXAG-3; XAG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lung disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTD 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 AA;
                                            Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       growth factor; breast disease; liver disease;
emphysema; wound healing; cancer; diagnosis; therapy;
                                                                                                                                         96WO-US13766
                                                                                                                                                                                        97WO-US14139
                                                                                                                                                                                                                                                                                                                                                                             /note= "Claim 12"
104..115
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label- Mat_protein
/note- "Claim 11"
25..44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- Sig_peptide
24..166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factor huXAG-3.
                                                                                                                                                                                                                                                                                                                                                       /label=
                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.8%;
100.0%;
                                            Endress
                                                                                                                                                                                                                                                                                                                                   "Claim 12"
                                                                                                                                                                                                                                                                                                                                                     Epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 593; DB 21; Pred. No. 4e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Query Match

DB 19;

Length 166;

4;

Sequence

166

AA;

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caused by viral hepatitis and toxic substances. They can also be used to stimulate or promote liver regeneration, e.g. after surgery. They can also be used to prevent and head damage to the lungs caused by various pathological states. They can be used to stimulate proliferation and differentiation and promote the repair of alveoli and bronchiolar epithelium to prevent, attenuate, or treat acute or chronic lung damage, e.g. emphysema, which results in the progressive loss of alveoli, and inhalation injuries, e.g. resulting from smoke inhalation and burns, that cause necrosis of the bronchiolar epithelium and alveoli. They can also be used to stimulate the proliferation and differentiation of breast tissue and could therefore be used to promote healing of breast tissue injury due to surgery, trauma or cancer. Antagonists can be used to treat hyperproliferative disorders, including cancer, in particular hepatocellular carcinoma, osteoclastoma, breast cancer, or or colon cancer. The products can also be used for detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cells, antibodies, and screening methods for identifying agonists and antagonists of huXAG-3 are provided. HuXAG polypeptides are growth factors and can be used to stimulate proliferation of cells. They can be used to stimulate the proliferation and differentiation of hepatocytes to alleviate or treat liver diseases and pathologies such as fulninant liver failure caused by cirrhosis, liver damage caused by viral hepatitis and toxic substances. They can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human growth factors also including huXAG-1 (see AAW3/844) and huXAG-2 (see AAW3/845). These proteins share homology with the XAG protein of Xenopus laevis, which is involved in embryogenesis XAG protein of Xenopus laevis, which is involved in embryogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This polypeptide comprises huXAG-3, a member of a novel far human growth factors also including huXAG-1 (see AAW37844)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 3A-B; 141pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated human XAG growth factor(s) - used to develop products for treating e.g. liver, lung or breast diseases or hyperproliferative disorders, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAV19157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is expressed in adult tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rpressed in adult tissue. huXAG-3 cDNA (see AAV19157) was
from a human small intestine cDNA library. Vectors, host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
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δÃ Вþ Qy 밁 Ş 밁 Matches 120 160 101 60 11 41 LLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEEALYKSKTSN 100 Local MFVDPSLTVRADIAGRYSNRLYTYEPRDLPLLIENMKKALRLIQSEL MFVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL pal Similarity 108; Conserv LLLVTVSSNLA--IAIK----KEKRP--PQTLSRGWGDDITWVQTYEEGLFYAQKSK Conservative 52.2%; 28; Mismatches Score 555; DB 1 Pred. No. 1e-52; 19; Indels 166 12; Gaps 59

Search completed: October Job time: 33 secs 9 2002, 16:40:04

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Result
No.
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Maximum Match 100%
Listing first 45 s
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Maximum DB
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Perfect score:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                    899
199
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C;Comment: This protein is C;Genetics: A;Gene: hAG-2

45	44	43	42	41	40	39	38	37	36	35	34	သ	32	31	30
76	76	76	76	76	76	76.5	76.5	78	78	78	78	78.5	78.5	78.5	78.5
7.1	7.1	7.1	7.1	7.1	7.1	7.2	7.2	7.3	7.3	7.3	7.3	7.4	7.4	7.4	7.4
1651	583	543	367	166	166	1025	985	1855	1853	1828	337	1570	1262	1033	917
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F88750	E75529	F64871	T39574	D86606	E72018	T10259	E69850	A59254	A46761	B59254	S06956	AC2012	I48855	A96714	T05430
protein vit-6 [imp	probable peptide A	oligopeptide-bindi	probable uracil ki	thioredoxin disulf	thioredoxin disulf	RNA-directed DNA p	formate dehydrogen	mysoin heavy chain	myosin heavy chain	mysoin heavy chain	segmentation prote	hypothetical prote	tripeptidyl-peptid	hypothetical prote	hypothetical prote

ALIGNMENTS

Anterior gradient-2 - human C;Species: Homo sapiens (man) C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999

#text_change 21-Jul-2000

cement gland gene XAG-2,

C; Accession: JE0350 R; Thompson, D.A.; Weigel, R.J.

Biochem. Biophys. Res. Commun. 251, 111-116, 1998 A;Title: hAG-2, the human homologue of the Xenopus laevis A;Reference number: JE0350; MUID:99009231 A;Accession: JE0350

A;Molecule type: mRNA A;Residues: 1-175 <THO> A;Cross-references: GB:AF007791; NID:g3779196; PIDN:AAC77358.1; PID:g3779197

coexpressed with estrogen receptor (ER) in

breast cancer c

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hypothetical protein Y57A10A.u - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000 C;Accession: T31643 R.Empe, R.
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-186 <WIL>
A;Cross-references: EMBL:AL117195; PIDN:CAB55026.1; CESP:Y57A10A.u
A;Experimental source: clone Y57A10A
C;Genetics:
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T31643
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                                                                                                            A; Reference number: A; Accession: T31643
                                                                                                                                submitted to the EMBL Data Library, September 1999 A; Reference number: Z21048
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Best Local Similarity 100.0%;
Matches 175; Conservative (
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;; Pred. No. 3.2e-74;
0; Mismatches 0;
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hypothetical protein YMR191w - yeast (Saccharomyces W;Alternate names: hypothetical protein YM9646.03 C;Species: Saccharomyces cerevisiae C;Date: 10-Feb-1995 #sequence_revision 12-May-1995 #C;Accession: S50919; S55721
                                                                                                                                                                                                                                                            RESULT
S50919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Q1u, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional complete genome sequence of Methanobacterium thermoautotrophicum Delta H:
A; Reference number: S50917
A; Accession: S50919
A; Molecule type: DNA
A; Residues: 1-458 < PEA>
                                                                                         R; Pearson, D.; Bowman, S. submitted to the EMBL Data Library,
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A;Experimental source: strain Delta H
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A; Residues: 1-150 < MTH>
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C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Sep-2000
C;Accession: D69100
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                                                                                                                                                                                                                                                                                                                                                        PTVIILDPS 129
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TGKNVFMVFSASWCPACQKLESETLQNTEVQRRLAEDFIAVKIDVDTSPALSSRYRIYGV 120
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ilarity 27.1%;
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Pred. No. 1.1e-10;
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Pred. No. 0.
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                                                                                                                                                                                                                                      cerevisiae)
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A;Cross-references: EMBL:Z47815; NID:g642280; PIDN:CAA87812.1; PID:g642283; MIPS: R;Gangloff, S.; McDonald, J.P.; Bendixen, C.; Arthur, L.; Rothstein, R. Mol. Cell. Biol. 14, 8391-8398, 1994
A;Title: The yeast type I topoisomerase Top3 interacts with Sgs1, a DNA helicase A;Reference number: A56359; MUID:95059068
A;Accession: $55721
                                                                                                                                                                                                                                                    A; Experimental source: strain CWLO29
R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, GNucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumc A; Reference number: A81500; MUID: 20150255
A; Accession: B81523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and A;Reference number: A72000; MUID:99206606
A;Accession: G72016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable disulfide bond isomerase - Chlamydophila pneumoniae (strains CWL029 C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-127, 'Y', 129-131, 'LALG', 136-249 <GAN>
A; Cross-references: EMBL: U22341; NID: 9726277; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-348 <ARN>
A;Cross-references: GB:AE001673; GB:AE001363; NID:g4377252; PIDN:AAD19071.1; PID:g437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
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C; Superfamily: Saccharomyces cerevisiae hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U22341; NID:9726277; PIDN:AAB60288.1; PID:9726278 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: G72016; B81523
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                                                                                                                          A; Experimental source: strain
                                                                                                                               A;Cross-references: GB:AE002251; GB:AE002161; A;Experimental source: strain AR39, HL cells
                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-348 < REA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                               A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGTFSAPLSFLDPSLL--ADLDEMIRN--YKYE 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HVQPVALKKLSQKDINFIRNLELFKIMK - - TQNEVVDETSAYYMEKPGSYIEFTISEFNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----ALKKV-----FAENKEIQKLAEQFVLLNLVYETTDKHLSPDGQYV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QLIWTQTYEEALYK --- SKTSNKPLMI ---- IHHLDECPHSQ ---
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Pred. No. 4.
Score 87;
Pred. No.
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                                                                                                                                                       NID: g7189833; PIDN: AAF38711.1;
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                                                                                                                                                                                                                                                                                                                                                                  O.; Hicke
G.; Salzbe
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                                                                                                                                                       PID:9718
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Local

Similarity

8.2%; 25.0%;

Conservative

26;

Mismatches

Indels

24;

Gaps

4.

DB 2;

Length 348;

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RESULT 7
S19188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuct
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences
A; Reference number: A86491; MUID:20330349
A; Accession: C86607
                                                                                                                                                                                                                                                                                                                                                                                                                       WiAlternate names: calmodulin-binding protein; myosin I heavy chain, 190K C;SpecLes: Gallus gallus (chicken)
C;Date: 31-Dec.1993 #sequence_revision 31-Dec.1993 #text_change 19-Jan-2001
C;Accession: S19188; A44359; B44359; S29249
R;Espreafico, E.M.; Cheney, R.E.; Matteoli, M.; Nascimento, A.A.; De-Camilli, submitted to the EMBL Data Library, Fabruary 1992
A;Description: Complete CDNA coding sequence of chicken brain p190, a calmodul
  R;Sanders, G.; Lichte, B.; Meyer, H.E.; Kilimann, M.W. FEBS Lett. 311, 295-298, 1992
A;Title: cDNA encoding the chicken ortholog of the mou
                                                                                              A; Molecule type: mRNA
A; Residues: 1-1688, 'R.,1690-1830 <ES2>
A; Residues: 1-2008, 'R.,1690-1830 <ES2>
A; Experimental source: brain
A; Note: sequence extracted from NCBI backbone (NCBIN:121153, NCBIP:121154)
A; Note: the codon CGC for residue 1689 is inconsistent with the codon AGC
A; Accession: B44359
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                                                          A; Molecule type: protein A; Residues: 155-164 <ES3>
                                                                                                                                                                                                                      A; Title: Primary structure and cellular localization A; Reference number: A44359; MUID:93107155 A; Accession: A44359
                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:Z11718
R;Espreafico, E.M.; Cheney, R.E.; Matteoli,
J. Cell Biol. 119, 1541-1557, 1992
                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-1830 <ESP>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-348 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YEEALYKSKTSNKPLMIIHHLDEC -- PHSQALKKVFAENKEIQKLAEQFVLLNLVY 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YQEALQKSKEAELPLLVIFSGSDWNGPCMKIRKEVLESPEFIKRVQGKFVCVEVEY 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YEEALYKSKTSNKPLMIIHHLDEC--PHSQALKKVFAENKEIQKLAEQFVLLNLVY 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YQEALQKSKEAELPLLVIFSGSDWNGPCMKIRKEVLESPEFIKRVQGKFVCVEVEY 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RCSLKQLKVLATLL - - - LSLSL - - - PTLEAAENRDS - - - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.2%;
25.0%;
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                      M.; Nascimento, A.A.; De Camilli, P.V.; Lar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.5;
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  mouse
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dilute
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R;Glaser, P.; Frang
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A; Residues: 1-1151 <GLA>
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A; Accession: AG1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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Best Local
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                                   LDNMKKALKLLKT
                                                                               YRTSAKKISGYKLYQTPK
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                                       204
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R.Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Ent D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E. A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-
A;Title: Comparative genomics of Listeria species,
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable peptidoglycan bound protein (I
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;645-666/Region: actin binding #status predicted F;765-909/Domain: neck #status predicted <NEC> F;7165-909/Domain: coiled coil #status predicted <COI> F;912-1420/Domain: coiled coil #status predicted <F;1421-1830/Domain: carboxyl-terminal domain #status predicted F;169/Binding site: ATP (Lys) #status predicted F;1735/Binding site: phosphate (Thr) (covalent) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X67251; NID:g63364; PIDN:CAA47673.1; PID:g63365 C;Comment: The neck domain comprises six approximately 23 residue tandem C;Superfamily: myosin MYO2; myosin motor domain homology C;Keywords: actin binding; ATP; brain; coiled coil; nucleotide binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AL592022; PIDN:CAC97511.1; PID:g16414795; GSPDB:GN00178 A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;72-752/Domain: myosin motor domain homology <MMOT>
F;163-170/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-1142, 1144-1830 <SAN>
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A;Accession: S29249
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                                                                                                                                                                                      961 VALDDSVAPVTVQYVDQNHKQIASPETLTGAYGEKFTAKQKKITNYTLVKTPANVSGTFN 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 567 KNKDTVYEEQIKVLKSSKKFKLLPELFQDEEKAISP 602
YETTDKHLSPDGQY-VPRIMEVDPSLTVRADITGRYSNR----LYAYEPADTALL----
                                                                                                                                                                                                                                               LARDTTVKPGAKK--DTKDSRPKLPQTLSRGWGDQLIWTQ
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                                                               EKAQTVTFVYQKVTAGN - - IIVDYVD-
                                                                                                                         EA------LYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVL----LNLV 141
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28.1%;
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                                                                                                                                                                                                                                                                                                                                         Score 84.5;
Pred. No. 26;
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Pred. No. 38;
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                                                                                                                                                                                                                                                                                                            51;
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                                                               -KNGEKLADSIVLTGKLNSS 1063
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                                                                                                                                                                                                                                                                                                            67;
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Voss, H.; W
      191
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K.D.; I
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C;Accession: T37859

R;Devilin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, February 1996

A;Reference number: Z21750

A;Accession: T37859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein YLR176c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein L9470.18
C;Species: Saccharomyces cerevisiae
C;Date: 23-Feb-1995 #sequence_revision 12-May-1995 #text_change
C;Accession: S51421
R;Wohldmann, P.
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A;Experimental source: strain 972h-; cosmid c17G8
                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-217 <DEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable transcription factor - fission yeast (Schizosaccharomyces
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-
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A;Gene: SGD:RFX1
A;Cross-references: {
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A; Residues: 1-771 <WOH>
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Best Local
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                                                                                                             14 HPSRRLTQG----
                                                                                                                                                                  Local Similarity
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les 47; Conserv
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                                  SRPKLPQTLSRGWGDQLIWTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENK 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D--TTVK------PGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEEALYKSKTSNKP 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSGSGP------HPSRRLTQGR----WYRKSRVAMEKIPVSAFLLLVALSYTLAR
   SPPF -- EVIETGWGEFDIMVRIF ---
                                                                        HTWRIFVEGVDGEDISKWVRK------VVFKL-----HDTYNNP---TRTIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NPPTAAKRTNTFPSIPSSTKKQKTSQEKRISSISRRNTQEIIAKQIAEN--NKSKTIEEY
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                                                                                                                                                   Conservative
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                                                                                                           --RWVRKSRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKD
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                                                                                                                                                                    Pred.
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Pred. No. 18;
                                                                                                                                                                  Score 83.5; Di
Pred. No. 4.1;
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FAPEAHEKALTFYHHLKLHPYGPRMEEMKASGG 130
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                                                                                                                                                 49;
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R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Wedler, submitted to the EMBL Data Library, January 1999
                                                                                                                                                                                      C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
                                                                                                                                                                                                         cell cycle protein kinase hskl – fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces nombo
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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A; Experimental source: strain 972h-;
     A;Cross-references: EMBL:AL035263; PIDN:CAB38417.1; GSPDB:GN00067; SPDB:SPBC776.12c A;Experimental source: strain 972h-; cosmid c776
                                       A; Molecule type: DNA
A; Residues: 1-479 < LYN>
                                                                                             A; Reference number: Z21944
A; Accession: T40683
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A;Gene: F19K16.21
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A; Residues: 1-918 <STO>
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A; Accession: C96829
A; Status: preliminary
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                                                                          A; Status: preliminary; translated
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                                                                                                                                                                     Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QTYEEALYKSKTSNKPLM----IIHHLDECPHSQALKKVFAENKEIQKLAEQFVLL---- 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PQSQILLEESSEYSLQTPESSGYKTSLQPNEKLEMTASQDSQPEQPK--SEAEESQPEDS 206
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Pred. No. 24;
41; Mismatches
                                                                           from GB/EMBL/DDB
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cell cycle protein kinase hsk1 (EC 2.7.1.-) - fissi C;Species: Schizosaccharomyces pombe C;Date: 28-Oct-1995 #sequence_revision 10-Nov-1995 C;Accession: S56143; T40682 R;Masai, H.; Miyake, T.; Arai, K. EMBO J. 14, 3094-3104, 1995 A;Title: hsk1(+), a Schizosaccharomyces pombe gene A;Reference number: S56143; MUID:95347336 A;Accession: S56143
RESULT
C70441
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A;Introns: 77/1; 92/2; 331/1
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol
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A; Accession: T40682
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A;Experimental source: strain JY2
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Wedler, H.; Kutzner, M.; Wambutt, R.
submitted to the EMBL Data Library, January 1999
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A; Residues: 1-507 <LYN>
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A; Residues: 1-507 <MAS>
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                  14
                                                                                                                                                                                                                                                83 LIWTQTYEEALYKSKTSNKP----LMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLL 138
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                                                                                                                                         DNLAYEKKDDDTAFDNS---
                                                                                                                                                                         -NLVYETTDKHLSPDGQYVPRIMFVDPSLTVRADITGRYSNRLYAY---EPADTALLLDN 194
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Pred. No.
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A; Experimental:
C; Genetics:
A; Gene: lplA
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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: C70441
                                                                                                                                                                                                                                                                                                  R; Leahey, A.M.; Charnas, L.R.;
Hum. Mol. Genet. 2, 461-463, 1
A; Title: Nonsense mutations in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 01-Dec-2000
C;Accession: S29069; I68621
C;Accession: S29069; I68621
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S29069
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                                                                                                                                                 A; Gene:
                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 883-912 <
                                                                                                                                                                                                                                                                                A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: S29069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Attree, O.; Olivos, I.M.; Okabe, I.; Bailey, Nature 358, 239-242, 1992
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A; Residues: 1-788 <A
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                                                                                                                                                                                     A;Cross-references:
                                                                                                                                                                                                                                           A; Status: preliminary; translated
                                                                                                                                                                                                                                                            A; Accession: I68621
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                               55 TVKPGAKKDTKDSRPK--LPQTLSRGWGDQLIWTQTYEEAL-YKS----KTS-NKPLMII 106
                                                                                                                                                 OCRL-1
TYKYDSKTDRWDSSGKCRVP----AWCDRILWRGTNVNQLNYRSHMELKTSDHKPVSAL 607
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GB:S62085; NID:g385336;
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I54349; MUID:93278398
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23.0%;
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Pred. No. 40;
32; Mismatches
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                                                                                                                                                                                       PIDN:AAB26926.1; PID:g385337
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Sear Job	Ф	Qy	ф	Qy	рь	δ
Search completed: October 9, 2002, 16:42:16 Job time : 23 secs	716 S	QY 185 PADTALLLDN 194	664 F	Qy 148 -HLSPDGQYVPRIMFVDPSLTVRADITGRYSNRLYAYE 184	Db 608 FHIGVKVVDERKYRKVFEDSVRIMDRMENDFLPSLELSRREEVFENVKFRQLQKGK 663	
16			PFEGYLEPNETVDISLDVYV 7	FVDPSLTVRADITGRYSNRLYAYE 18	NDFLPSLELSRREFVFENVKFRQLQKGK 6	QFVLLNLVYETTDK 1:
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Minimum DB
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83.5
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Gapop 10.0 ,
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1063
  SwissProt_40:*
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NP77. XENLA
YM51_YEAST
MY5A_CHICK
RFXL_YEAST
YD67_SCHPO
OCRL_HUMAN
TOP2_PLAFK
YTH6_RHOER
YM51_YEAST
ERA_HELPJ
CBP1_ORYSA
AROEE_BACSU
TPP2_MOUSE
MY5A_RAT
                                                                MY5A_HUMAN
PO21_NASVI
OPPA_ECOLI
U520_CAEEL
TREZ_MYCTU
NTC3_MOUSE
 SN_MOUSE
Z03_MOUSE
TATD_ECOLI
GM13_RAT
POL_HV2CA
VIT6_CAEEL
YEG7_YEAST
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MY5A_MOUSE
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(without alignments)
613.556 Million cell updates/sec
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P55868 xenopus J
P55869 xenopus J
P55869 xenopus J
P4293 saccharon
Q02440 gallus ga
P48743 saccharon
Q10319 schizosac
Q10196 homo sapi
P41001 plasmodiu
P43484 rhodococc
Q05050 saccharon
Q251W0 helicobac
P54374 bacillus
Q64514 mus muscu
Q9416 rattus nc
Q99416 rattus nc
Q99417 nasonia v
P23843 escherich
Q90290 caenorhat
Q10769 mycobacte
Q6230 mus muscu
Q6230 mus muscu
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Q94117 human imm
P18446 caenorhat
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P34736 pichia st
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0 gallus gall
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1 homo sapien
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72	72	72	72	72	72.5	72.5	72.5	73	73	73.5	73.5	
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ZO3_CANFA	YP22_YEAST	YQE4_CAEEL	YKJ0_YEAST	UL95_HSV6U	DMSA_RHOCA	YYAL_BACSU	KTHY_METJA	UNC7_CAEEL	GUN_CLOSA	CSE1_PAGMA	YP65_CAEEL	
O62683 canis famil		Q17529 caenorhabdi			Q52675 rhodobacter				P15704 clostridium		Q09214 caenorhabdi	

ALIGNMENTS

Qy 1	Qу	Qу	Query M Best Lo Matches	SQ SE	FT SI					CC C								RC TI				00 Am				DT 01	XAG_XENLA
	90 EEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLA-EQFVLLNLVYETTDKH 148 ::: : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::	39 AFILLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTY 89 ::	y Match 42.1%; Score 448; DB 1; Length 183; Local Similarity 49.4%; Pred. No. 1e-34; hes 88; Conservative 29; Mismatches 51; Indels 10; Gaps 3;	Α̈́Α,	L 1 18 POTENTIAL.	76752; AAB18819.1;	send an email to license	http://www.i	use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial	European Bioinformatics Institute. There are no restrictions on	This SWISS-PROT entry is copyright. It is produced through a collaboration	-!- SIMILARITY: HIGH, TO AENORGO NE//.	TISSUE SPECIFICITY: EXPRESSE	•	roposterior patterning.";	"A sticky problem: the Xenopus cement gland as a paradigm for	Sive H., Bradley L.:	TISSUE=Cement gland;	SEQUENCE FROM N.A.	NCBI_TaxID=8355;	opus.	EuwaryOta, meta20a, Chordata, Craniata, Vertebrata, Eucereoscomi, Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;	wotagoa: Chordata: Craniata: Vortobrata:	YAG.	(Rel.	1997 (Rel. 35, Crea) 1997 (Rel. 35, Last	ENLA XAG XENLA STANDARD: PRT: 183 AA.

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RESULT
NP77_XE
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Best Local :
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P55869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal.
SIGNAL
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                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-OCT-1996 (Rel. 34, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
Hypothetical 52.2 kDa protein in SGS1
YMR191W OR YM9646.03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-Cement gland;
TISSUE-Cement;
Aberger F., Schueren C., Lepperdinger G., Richter K., Grushmitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-I- SUBCELLULAR LOCATION: Secreted (Probable).
-I- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVEL IN CEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998
15-JUL-1998
                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetaceae; Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative secreted
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STRAIN-S288C
Pearson D., I
                           SEQUENCE FROM N.A
                                                                                                                                                                   P42933;
                                                                                                                                                                              YM51_YEAST
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Bowman S.,
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36, Last sequence update
36, Last annotation upd
protein NP77 precursor.
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Pred. No. 9.7e-34;
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PUTATIVE SECRETED
                                                                            Saccharomycotina;
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 B.G.,
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RESULT 4
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01-JUN-1994 (Rel. 2
16-OCT-2001 (Rel. 4
Myosin Va (Myosin 5
heavy chain P190) (
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MEDLINE=93012002; PubMed=1383040;
Sanders G., Lichte B., Meyer H.E., Kilimann M.W.;
"cDNA encoding the chicken ortholog of the mouse dilute
Sequence comparison reveals a myosin I subfamily with co
                                                                                                                                    Gallus gallus (Chicken)
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                                                 TISSUE-Brain;
                                                           SEQUENCE FROM N.A.
                                                                                                             Archosauria;
                                                                                                                        Eukaryota;
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                                                                                    NCBI_TaxID=9031;
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; U22341; AAB60288.1;
S0004803; YMR191W.
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FVTW -> LALG (IN RE
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Pred. No. 1
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Phasianinae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Cell Biol. 119:1541-1557(1992).

-i- FUNCTION: PROCESSIVE ACTIN.-BASED MOTOR THAT CAN MOVE IN LARGE STEPS APPROXIMATING THE 36-NM PSEUDO-REPEAT OF THE ACTIN FILAMI MAY BE INVOLVED IN MELANOSOME TRANSPORT, OR ALTERNATIVELY, IT MER REQUIRED FOR SOME POLARIZATION PROCESS INVOLVED IN DENDRITE FORMATION (BY SIMILARITY).

-i- SUBUNIT: MAY BE A HOMODIMER, WHICH ASSOCIATES WITH MULTIPLE CALMODULIN OR MYOSIN LIGHT CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          terminal FEBS Lett
                                                                                                                                                                                                                                                                                                                         SMART; SM00015; IQ; 6.
SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01843; DIL; 1.
Pfam; PF00612; IQ; 6.
Pfam; PF00063; myosin_head; 1
PRINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X67251; CAA47673.1; -. EMBL; Z11718; CAA77782.1; -. HSSP; P08799; IMMG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Espreafico E.M., Cheney R.E., Matteoli M., Nascimento A.A., de Camilli P.V., Larson R.E., Mooseker M.S., et al. "Primary structure and cellular localization of chicken brain myosin-V (p190), an unconventional myosin with calmodulin light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                               PROSITE; PS50096;
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InterPro; IPR001609; myosin_head.
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63 DTKDSRPKLPQTLSRGWGDQLIWTQTYEEALY-KSKTSNKPLMIIHHLDECPH--SQALK 119
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                                                                                                                                                                                                                                                                                     coil;
                                                                                                                                                                                                                                                                                                 Repeat; ATP-binding;
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                                                    Similarity
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t. 311:295-298(1992).
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COILED COIL (POTENTIAL).
DILUTE.
ATP (BY SIMILARITY).
ACTIN-BINDING (POTENTIAL).
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E -> EQ (IN REF. 2).
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0538B278DFC09F6E CRC64;
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11;
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YD67_SCHPO
Q10319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical SEQUENCE 8
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YLR176C OR L9470.18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                          NPPTAAKRTNTFPSIPSSTKKQKTSQEKRISSISRRNTQEIIAKQIAEN--NKSKTIEEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KNKDTVYEEQIKVLKSSKKFKLLPELFQDEEKAISP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity
47; Conserv
                                                                                                                                                                                             158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -VFAENKEIQKLAEQFVLLNLVYETTDKHLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  811 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 33, (Rel. 36, IRel. 40, IRel. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AB972;
                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YLR176C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 33, Created)
. 36, Last sequence . 40, Last anno
                                                                                                                                                                                                                                                                                     LDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSPDGQY 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---HPSRRLTQGR----WVRKSRVAMEKIPVSAFLLLVALSYTLAR 52
                                                                                                                                                                                                                                                                                                                                                                      PGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEEALYKSKTSNKP 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.9%;
25.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90583 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
protein in CBF5-DKA1 intergenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 84;
                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116A88B7DDE4FBF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.
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                         217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no restrictions in as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                         B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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01-OCT-1996 (Rel. 3
01-OCT-1996 (Rel. 3
Hypothetical 24.9 kl
SPAC17G8.07.
                                                                                                                                                                                                     HSK1_SCHPO PRT; 5
P50582; 094678;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence up
16-0CT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A., Wals
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
-i-SIMILARITY: TO HUMAN AF9 AND ENL AND YEAST TRANSCRIPTION
INITIATION FACTOR TFIIF SMALL SUBUNIT (TFG3/ANC1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomye
Schizosaccharomycetales;
Schizosaccharomyces.
MEDIINE-95347336; PubMed-7621824;
Masai H., Miyake T., Arai K.-I.;
"hskl+, a Schizosaccharomyces pombe gene related to Saccharomyces cerevisiae CDC7, is required for chromosomal replication.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                             SEQUENCE FROM N.A.
                                                                                                                        Schizosaccharomyces.
                                                                                                                                    Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                Cell cycle protein kinase hskl (EC HSK1 OR SPBC776.12C.
                                                                                                                                                                                                                                                                                       SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-4896;
                                                                                                        NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
                                                                                                                                                                                                                                                                                                                                                  181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 HPSRRLTQG-----RWVRKSRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKD 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity es 42; Conser
                                                                                                                                                                                                                                                                                                                                                                                                         LVESVQYEEIVFNEPFEYTYKLLSQNPIGDGH------GLAVESEPDHPFSQQLEQ 180
                                                                                                                                                                                                                                                                                                                                                DEADKLDFAIQEVKKTIEMYKQQV
                                                                                                                                                                                                                                                                                                                                                                             YEPADTALLLDNMKKALKLLKTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                     EIQKLAEQFVLLNLVYETTDKHLSP----DGQYVPRIMFVDPSLTVRADITGRYSNRLYA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPPF--EVIETGWGEFDIMVRIF----FAPEAHEKALTFYHHLKLHPYGPRMEEMKASGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRPKLPQTLSRGWGDQLIWTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTWRIFVEGVDGEDISKWVRK------VVFKL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z69795; CAA93690.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
17 AA; 24946 MW; A274C2AFB0620D7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34, Created)
34, Last sequence update)
34, Last annotation updat
kDa protein C17G8.07 in c
                                                                           (LONG FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 83.5;
                                                                                                                                                                                                                                                                                                                                                                             206
                                                                                                                                                                                                                                                                                                                                                204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ed. No. 1.1;
Mismatches
                                                                                                                                                                                               ion update)
2.7.1.-).
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                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                        507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
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RESULT 8
OCRL_HUMAN
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Best L
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                            HUMAN STANDARD; PRY; OCTL_HUMAN STANDARD; OPUJGS; Q15774; Q9UMA5; Q01968; Q15684; O60800; Q9UJGS; Q15774; Q9UMA5; Q1-JUL-1993 (Rel. 26, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Inositol polyphosphate 5-phosphatase OCRL-1 (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
NP_BIND
BINDING
ACT_SITE
VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBO
                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00108; PROTEIN_KINASE_ST; 1
PROSITE; PS50011; PROTEIN_KINASE_DOM;
Cell cycle; Cell division; Serine/thre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; Q16539; 1WFC.
InterPro; IPR000719; Euk_pkinase
InterPro; IPR002290; Ser_thr_pki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL035263; CAA22885.1; EMBL; AL035263; CAB38417.1;
                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00069; pkinase; PROSITE; PS00107; PROTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between
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SEQUENCE
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                                                                                                                                                                                                                                                                                                 436
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                                                                                                                                                                                                                                                                      195
                                                                                                                                                                                                                                                                                                                          139
                                                                                                                                                                                                                                                                                                                                                                             83 LIWTQTYEEALYKSKTSNKP----LMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLL 138
                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                 Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHORT FORM;
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nitted (JAN-1999) to the EMBL/GenBank/DDBJ databases FUNCTION: REQUIRED FOR CHROMOSOMAL REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a cen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. 14:3094-3104(1995).
                                                                                                                                                                                                                                         RKRSI 494
                                                                                                                                                                                                                                                                     MKKAL 199
                                                                                                                                                                                                                                                                                                  DNLAYEKKDDDTAFDNS-----FGETSFEKDEDLTAKHLSHILDFKEQEETDEPTSLSK
                                                                                                                                                                                                                                                                                                                         -NLVYETTDKHLSPDGQYVPRIMFVDPSLTVRADITGRYSNRLYAY---EPADTALLLDN 194
                                                                                                                                                                                                                                                                                                                                                   ILWASCGSASIYKEKLRHKPSQEERLCLDFLEKCLELDCNKRISAE----EALDHDFLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D50493; BAA09087.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A. (LONG AND SHORT FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rajandream M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 433
129 129
129 129
216 216
92 119
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; PROTEIN_KINASE_ATP;
                                     Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           58407
                                                                                                                                                                                                                                                                                                                                                                                                                   22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 7.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _thr_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                        24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

MISSING (IN SHORT ISOFORM).

M9; 04970E58218441EE CRC64;
В)
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 83;
Pred. No.
                                        Craniata; Vertebrata; Catarrhini; Hominidae;
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3.7;
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                                         Hominidae;
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£ outstation -
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Zhang X., Hartz P.A., Philip E., Racusen L.C., Majerus F "Cell lines from kidney proximal tubules of a patient wisyndrome lack OCRL inositol polyphosphate 5-phosphatase accumulate phosphatidylinositol 4.5-bisphosphate."; 13. Biol. Chem. 273:1574-1582(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
Mistry S.
                                                              VARIANTS LS GLN-500 AND GLN-524.
MEDLINE-98293952; PubMed-9632163;
Kawano T., Indo Y., Nakazato H., Shimadzu N
"Oculocerebrorenal syndrome of Lowe: three
derived from three patients with different
Am. J. Med. Genet. 77:348-355(1998).
                                                                                                                                                    WARIANTS IS TYR-375; GLN-500; ASP-508 ANI
MEDLINE-98347141; PubMed-9682219;
Lin T., Orrison B.M., Suchy S.F., Lewis I
"Mutations are not uniformly distributed
Lowe syndrome patients.";
                                                                                                                                                                                                                                                                                                                                                                                         Zhang X., Jefferson A.B., Auethavekiat V., Majerus P
"The protein deficient in Lowe syndrome is a
phosphatidylinositol-4,5-bisphosphate 5-phosphatase.
Proc. Natl. Acad. Sci. U.S.A. 92:4853-4856(1995).
[7]
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-95281554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nonsense mutations in the OCRL-1 gene oculocerebrorenal syndrome of Lowe."; Hum. Mol. Genet. 2:461-463(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Brain;
MEDLINE-97201100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The Lowe's oculocerebrorenal syndrome gene encodes a homologous to inositol polyphosphate-5-phosphatase."; Nature 358:239-242(1992).
           Kubota T., S
Fukushima Y.
                                WARIANT LS ARG-522.
MEDLINE-99002770; F
                                                                                                                                                                                                                                                      Lin T., Orr
Lewis R.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Attree O., Olivos I.M., Okabe I., E
Lewis R.A., McInnes R.R., Nussbaum
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                                                                                                                                                                                                                                            "Spectrum of mutations
                                                                                                                                                                                                                                                                             MEDLINE=97342912;
                                                                                                                                                                                                                                                                                        VARIANTS LS T-367
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98104142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Physical mapping
 Identification of two
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.A., Nussbaum R
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                   PubMed=9788721;
i A., Arakawa K.,
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owe: three mutations in
different phenotypes.";
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Pfam; PF00620; RhoGAP; 1
SMART; SM00128; IPPC; 1.
SMART; SM00324; RhoGAP;
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splicing; Disease mutation GAP DOMAIN.

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372

372 367 357

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SYNDROME

SYNDROME)

367 357

/FTId=VAR_010169.
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/FTId=VAR_010170.
MISSING (IN LOWE S:
/FTId=VAR_010171.
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IPR000198; IPR000300; IPPc

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Kammerer S
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                                                                                                                                                                                                                                                                           LUNG, PLACENTA, AND KIBRUDHING.

DISEASE: DEFECTS IN OCRL ARE THE CAUSE OF LOWE'S OCULOCE
SYNDROME, A DISEASE CHARACTERIZED BY HYDROPHTHALMIA, CAT
MENTAL RETARDATION, VITAMIN D-RESISTANT RICKETS, AMINOAC
AND REDUCED AMMONIA PRODUCTION BY THE KIDNEY.

SIMILARITY: BELONGS TO THE INOSITOL-1,4,5-TRISPHOSPHATE
5-PHOSPHATASE TYPE II FAMILY.

SIMILARITY: CONTAINS 1 GAP DOMAIN.
L; M88162; AAA59964.1; ALT_IN

L; U57627; AAB03839.2; -.

L; AL022162; CAA18150.1; -.

L; AL022162; CAA18151.1; -.

L; Z73496; CAA97842.1; -.

L; S62085; AAB26926.1; -.
                                                                                                                                                                                            European Bioinformatics Institute.
                                                                                                                                                                                                                                                                DATABASE: NAME=Lowe Syndrome mutation database; WWW="http://www.nhgri.nih.gov/DIR/GDRB/Lowe/ocrll_mut_db.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALTERNATIVE PRODUCTS: 2 ISOFORMS; PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRISPHOSPHATE TO INOSITOL 1,4-BISPHOSPHATE AND INOSITOL 1,3,4,5-TETRAKISPHOSPHATE TO INOSITOL 1,3,4-TRISPHOSPHATE. MAY FUNCTION LYSOSOMAL MEMBRANE TRAFFICKING BY REGULATING THE SPECIFIC POOL (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHATIDYLINOSITOL 4,5-BISPHOSPHATE THAT IS
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                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a sen the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                     non-profit institutions as long and this statement is not removed. requires a license agreement (See an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIFICITY:
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Satre V., Lerouge E.,
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54:199-202(1998).
                                                                                    AAA59964.1; ALT_INIT
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PubMed=10767176;
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SEQUENCE
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         MEDLINE-94316496;
                                           Plasmodium falciparum
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                                                                                                                                                               639 SKDSVTILNS 648
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                                                                                                                                                                                                                                                                                                           Local Similarity
nes 45; Conserv
                                                                                                                                                                                PADTALLLDN 194
                                                                                                                  PLAFK
                                                                                                                                                                                                                   -HLSPDGQ----YVPRIM------FVDPSLTVRADITGRYSNRLYAYE 184
                                                                                                                                                                                                                                     FHIGVKVVDE----RRYRKVFEDSVRIMDRMENDFLPSLELSRREFVFENVKFRQLQKGK
                                                                                                                                                                                                                                                       HHL-----DECPHSQALKKVFAENKEIQKLAE----
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PubMed=8041616;
eese S., Goman M.,
                                                                       31, Created)
31, Last sequence update)
39, Last annotation update)
II (EC 5.99.1.3).
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                                                                                                                                                                                                                                                                                                                    Score 81.5;
Pred. No. 1
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H -> R (IN LOWE
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                                                                                                                                                                                                                                                                                                                                              /FTId=VAR_010189.
G -> E (IN REF. 3 AND 4).
; 90B6F6CDDD354BFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                        A -> P (IN LOWE SYNDROME)
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N -> D (IN LOWE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VAR_010179.
R -> Q (IN LOWE SYNDROME)
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                                            Haemosporida;
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Johnson
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D., Horrocks
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RESULT 10
YTH6_RHOER
ID YTH6_RHOER
AC P43484;
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Best Local
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01-OCT-1996
16-OCT-2001
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ACT_SITE
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SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- MISCELLANEOUS: EUKARYOTIC TOPOISOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00615; CCAATSUBUNTA. PRINTS; PR00418; TPIZFAMILY. ProDom; PD000616; DNA_topoisoII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X79345; -; NOT_ANNOTATED_CDS. HSSP; P06786; 1BGW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
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-1- MISCELLANBOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES RELAX ONLY NEGATIVE SUPERCOILS.
-1- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00204; DNA_topoisoIV; 1. Pfam; PF00521; DNA_topoisoIV; 1.
Hypothetical Rhodococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                      1016 TLTTT--
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                                                                                                                                                                                                                                                                                                     189 ALLLDNMKKALKLLKTE
                                                                                                                                                                                                                                                                                                                                                                                                 140 LVYETTDKHLSPDGQYVPRIMFVDPSLTVRADITGRYS-----NRLYAYEPADT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 WTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQ-----FVLLN 139
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SM00434; TOP4c;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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IPR001241; DNA_topoisoII.
IPR002205; DNA_topoisoIV.
IPR003594; HATPase_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Topoisomerase: DNA-binding; ATP-binding; Nuclear 144 149 ATP (POTENTIAL). 830 BNA CLEAVAGE (BY SIMILARITY). 271 281 POLY-ASN. 308 316 POLY-ASN.
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1227
1398
                   (Rel. 32, Created)
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1 37.5 kDa protein in thcR 5'region
erythropolis
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21.9%;
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5; Mismatches
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Pred. No. 18;
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POLY-LYS.
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RESULT 11
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Best Local S
Matches 31
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SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
SUBMIN S., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: TO YEAST VKINSON
                                                                                                                                                                  YMR031C OR YM99/J.va...
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharyota; Fungi; Ascomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dehydrogenase.";
J. Bacteriol. 177:676-687(1995)
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"The first characterization of a eubacterial proteasome: the complex of Rhodococcus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical SEQUENCE 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U26421; AAC45738.1; -.
EMBL; U17130; AAC45747.1; -.
InterPro; IPR004347; DUE245.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-NI86/21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FVDPSLTVRADITGRYSNRLYAYE--PADTALLLDNMKKALKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPVTAVHHISHDPTLRA-TVALADGRELTGLALQRIYLDRV----DKFMSAEGNDDPRV- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSPDGQYVPRIM 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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29.5%;
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Last annotation update)
protein in TAP42-CYK2 i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 80; DB 1; Length 339; Pred. No. 4.2;
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P-450 system a
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RESULT 12
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Q9ZLW0;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE-99120557; PubMed-9923682;

Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P. Alm R.A., Noonan B., Guild B.C., deJonge B.L., Carnel G., Smith D.R., Noonan B., Gria-Nickelsen M., Mills D.M., Ives C., Tummino P.J., Caruso A:, Uria-Nickelsen M., Mills D.M., Ives C., Mills D.M., Mills D.M., Ives C.,
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collar between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions
                                                                     or send an email to
                                                                                                                                                                                                                                                                          gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                           EMBL; AE001480;
HSSP; P06616; 11
                                                                                                                             the European Bioinformatics Institute.
                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                 -!- FUNCTION: BINDS BOTH GDP AND GTP, HAS AN INTRINSIC GTPASE AND IS ESSENTIAL FOR CELL GROWTH (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ERA/TRME FAMILY OF GTP-BINDING
                                                                                                                                                                                                                                                             Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ERA OR JHP0466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Last sequence up 16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; 249213; CAA89146.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                         "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter
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                                                                                                                                                                                                                                                             c pathogen Helicobacter
397:176-180(1999).
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38; Conser
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                                                                      an email to license@isb-sib.ch)
                                                                                                 non-profit institutions as long and this statement is not removed.
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Pred. No.
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on update)
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                                                                                                           There are no restrictions ong as its content is in
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KH_TYPE_2

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RESULT 13
CBP1_ORYSA
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Best Local S
Matches 25
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01-0CT-1994
01-0CT-1996
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00013; KH
PROSITE; PS50823;
GTP-binding; RNA-
                                                                                                                       MEROPS; S10.001; -.
                                                                                                                                                                                                                                                                                                                                         Biochim. Biophys. Acta 1199:311-
-:- CATALYTIC ACTIVITY: Release
                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV. YUKIHIKARI;
MEDLINE-94213891; PubMed-8161571;
Washio K., Ishikawa K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Last annotation update)
Serine carboxypeptidase I precursor (EC 3.4.16.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
PROSITE; PS00131; CARBOXYPEPT_SER_SER; 1.
PROSITE; PS00342; MICROBODIES_CTER; 1.
PROSITE; PS00560; CARBOXYPEPT_SER_HIS; 1.
Hydrolase; Carboxypeptidase; Glycoprotein; Zymogen;
SIGNAL 1 25 POTENTIAL.
PROPEP 26 36 POTENTIAL.
                                                                           Pfam; PF00450; serine_carbpept;
PRINTS; PR00724; CRBOXYPTASEC.
                                                                                                                                                  EMBL; D17586; BAA04510.1;
PIR; S43516; S43516.
                                                                                                                                                                                                                                                                                                                                                                   "Cloning and sequencing of the gene rice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa
                                                                                                 InterPro; IPR000379; Est_lip_thioest_actsite.
InterPro; IPR001563; Serine_carbpapt.
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                                                                                                                                                                                                                                                                                         PTM: THREE DISULFIDE BONDS ARE PRESENT (POTENTIAL) SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10; ALSO SERINE CARBOXYPEPTIDASE FAMILY.
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                                                                                                                                         P08819;
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(Rel. 30, Last sequence unit (Rel. 34, Last annotation)
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yta; Liliopsida; Poales; Poaceae;
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P54374;

01-OCT-1996 (Rel. 34, Creat

01-OCT-2996 (Rel. 34, Last

16-OCT-2001 (Rel. 40, Last

Shikimate 5-dehydrogenase (
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Sato T., Takeuchi M.;
Submitted (MAY-1996) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus subtilis.
Bacteria; Firmicutes;
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pfam; PF01488; Shikimate_DH; 1.
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Q64514;
Q1-NOV-1997 (Rel. 35, Created)
Q1-NOV-1997 (Rel. 35, Last seque
16-OCT-2001 (Rel. 40, Last annot
Tripeptidyl-peptidase II (EC 3.4
                                                                                                                                                 Hydrolase;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alternative splicing.";
Biochem. J. 304:517-523(1994).
-!- CATALYTIC ACTIVITY: Release of an N-terminal tripeptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=LEADEN X A1;
MEDLINE=95091686; Po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                         PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00136; SUBTILASE_
PROSITE; PS00137; SUBTILASE_
PROSITE; PS00138; SUBTILASE_
                                                                                                                                                                                                                                                                                                     Pfam; PF00082; Peptidase_S8;
                                                                                                                                                                                                                                                                                                                                                                 EMBL; X81323; CAA57103.1; HSSP; P00782; 2SBT.
                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                              MGD; MGI:102724; Tpp2.
InterPro; IPR000209; Peptidase_S8.
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SUBCELLULAR LOCATION: Cytoplasmic.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBTILASE FAMILY.
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                            AGSLTLSKTELGKKAGQSAAKRQGKFKKDVIPVHYYL-----IPPPTKIKNGSKDKE 1021
                                                        AGTLSGSGPHPSRRLTQGRWVRKSRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAK---
-----KDTKDSRPKLPQTLSRGWGDQLIWTQTYEEALYKSKTSNKPLMI--IHHLDECP 113
                                                                                                       Similarity
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44 CHARGE RELAY SYSTEM (BY SI
264 264 CHARGE RELAY SYSTEM (BY SI
449 449 CHARGE RELAY SYSTEM (BY SI
449 449 CHARGE RELAY SYSTEM (BY SI
985 997 MISSING (IN SHORT ISOFORM)
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SUBTILASE_HIS; 1.
SUBTILASE_SER; 1.
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Search completed: October 9, 2002, 16:40:31 Job time: 15 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd

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O9na78 caenorhabdi
O9n587 caenorhabdi
O27777 methanother
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O9af04 frankia sp.
O92952 listeria in
O92912 listeria in
O92918 caenorhabdi
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ALIGNMENTS

RESULT 1 Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF038451; AACR2614.1; -.
EMBL; AF007791; AAC77358.1; -.
EMBL; AF008867; AAF22484.1; -.
EMBL; BC015503; AAH15503.1; -. XAG-2, i lines."; 095994 PRELIMINARY; PRT; 175 AA.
095994;
01-MAY-1999 (TremBLrel. 10, Created)
01-MAY-1999 (TremBLrel. 10, Last sequence update)
01-DEC-2001 (TremBLrel. 19, Last annotation update)
SECRETED CEMENT GLAND PROTEIN XAG-2 HOMOLOG (ANTERIOR GRADIENT (XENEPUS LASVIS) HOMOLOG). SEQUENCE FROM N.A.
Zhang J.S., Smith D.I.;
"Human homolog of XAG is differentially expressed in tumors.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases. MEDLINE-99009231; PubMed-9790916; Thompson D.A., Weigel R.J.; "hAG-2, the human homologue of the Xenopus laevis cement gland gene "hAG-2, is coexpressed with estrogen receptor in breast cancer cell Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. SEQUENCE HAG-2/R OR HAG-2/C TISSUE=COLON ADENOCARCINOMA; SEQUENCE FROM N.A. Biochem. Biophys. Res. Commun. 251:111-116(1998). TISSUE=BREAST SEQUENCE FROM N.A. NCBI_TaxID=9606; AA: 19979 MW; F271B1BD377BEE11 CRC64;

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RESULT OR RESULT
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                                                                                                                   Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Alzawa K., Izawa M., Nishi K., Klyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Bolfelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Bakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Bolfelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
A Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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01-NOV-1998
01-DEC-2001
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SEQUENCE FROM N.A.
TISSUE-PANCREAS;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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STRAIN-BALB/C; TISSUE-INTESTINE;
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  SEQUENCE
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                                                    Nature
                                                                                  "Functional annotation
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Pred. No. 4.1e-80;
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EMBL; AF044262; AAC72705.1; ---
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                           Hypothetical SEQUENCE 1
                                                                                                                                                                 Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC008913; AAH08913.1; -.
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                                               PDGQYVPRIMEVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLA-EQFVLLNLVYETTDKHLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVLLCSVLGEAALRKPKRQAGATDTNGAAKSEPAPVKTKGLKTLDRGWGEDIEWAQTYEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVALSYTLARDTTVKP------GAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H.L.,
                      HHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKH--LSPDGQYVPRIMFVDP 164
                                                                                                                                                                                                                                                                                                                                                                                                          PDGHYVPRVIFIDPSLTVRSDLKGRYGNKLYAYDADDIPELITNMKKAKSFLKTEL
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                                                                                                                                           al protein.
172 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       324051; PubMed=2752418; Hattori K., Weintraub H.;
                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus.
                                                                                                                                                                                                    AND ADENOCARCINOMA;
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                                                                                                                                           19228 MW;
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50.68;
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Last annotation updat
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Pred.
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Pred. No. 7
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                                                                                                                                         5C9DDA6D5A7C4BDF CRC64;
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                                                                                                                   DB 4;
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RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Fruno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Hofmann M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storoh K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashiyaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                 MGD; MGI:1913323; Watterget.
InterPro; IPR000886; ER_target.
InterPro; IPR000063; Thiored.
InterPro; IPR000064; ER_TARGET; UNKNOWN_1.
PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
19048 MW; 5B91FC9BE12C5E44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-C578L/6J; TISSUE-EMBRYO, AND KIDNEY;
STRAIN-C578L/6J; TISSUE-EMBRYO, AND KIDNEY;
MEDLINE-21085660; PubMed-11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Kawai J., Shinagawa A., Fukunishi Y., Konno H., Adachi J., Fukuda Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka
                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (APR-2001) to the EMBL,
EMBL; AK003481; BAB22811.1; -
EMBL; AK002862; BAB22413.1; -
EMBL; BC006857; AAH06857.1; -
EMBL; BC006857; AAH06857.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9CQU0;
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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111
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                                                                                                                                                                                                                                   Pocat
                                                                                                                                          SFLLLITSS
                                                                                                                                                                              AFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEEALYKSKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLL
 PRILFLDPSGKVRPEIINESGNPSYKYFYVSAEQVVQGMKEAQERL
                                   PRIMFYDPSLTYRADITGRYSNRLYAYEPADTALLLDNMKKALKLL
                                                                     SGLPLMVIIHKSWCGACKALKPKFAESTEISELSHNFVMVNLEDEEEPRDEDFSPDGGYI 110
                                                                                        SNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNL--VYETTDKHLSPDGQYV 156
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                                                                                                                                                                                                                  Conservative
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Rodentia;
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Last annotation update)
N CDNA 0610040B21 GENE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                               Score 224.5;
Pred. No. 4e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vert
Sciurognathi;
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                                                                                                                                                                                                                  Mismatches
                                                                                                                                          DGR----TGLGKGFGDHIHW-RTLEDGKKEAAA
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                                                                                                                                                                                                                                 4e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202
                                                                                                                                                                                                                  58;
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                  Length 170;
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; Murinae; Mus
 156
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Best Local S
Matches 54
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Ricaffente J.Y., Wentland M.A., Le
"Large-scale concatenation cDNA se
Genome Res. 7:353-358(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAY-2001) to the EMBL/GenBank/DDBJ EMBL; AF131758; AAD20035.1; -. EMBL; BC001493; AAH01493.1; -. EMBL; BC008953; AAH01493.1; -. Interfro; IPR000063; Thiored. PROSITE; PS00194; THIOREDOXIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                Q9NA78;
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-COLON
Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-KIDNEY ADENOCARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=97264341; PubMed=9110174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-96207227; PubMed-8619474;
                                                                                                                                                        Q9NA78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical SEQUENCE 1
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"A 'double adaptor' met
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Y57A10A.23 PROTEIN Y57A10A.23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSRPKLPQT------LSRGWGDQLIWTQTYEEALYKSKTSNKPLMII 106
                                                                                                                                                                                                                                                                                       SGKVHPEIINENGNPSYKYFYVSAEQVVQGMKEAQERL
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                                                                                                                                                                                                                                                                                                                                                                                            IHKSWCGACKALKPKFAESTEISELSHNFVMVNLEDEEEPKDEDFSPDGGYIPRILFLDP
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d (FEB-1999)
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172 AA; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADENOCARCINOMA;
                                                                                                                                                           PRELIMINARY;
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method for improved
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Primates;
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to the
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KDA PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
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Last sequence up
Last annotation
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Catarrhini;
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Science 282:2012-2018(1998).
EMBL; ALIT7195; CAB55026.1; -.
InterPro; IPR000063; Thiored.
SEQUENCE 186 AA; 21467 MW;
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Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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Rhabditidae; Pel
NCBI_TaxID=6239;
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Eukaryota; Metazoa; Nematoda;
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EMBL; AC006642; AAF39830.1;
InterPro; IPR000886; ER_target.
InterPro; IPR000063; Thiored
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STRAIN-BRISTOL N2
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                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                     "Genome sequence of the nematode C. elegans: a plinvestigating biology. The C. elegans Sequencing Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                              STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
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                                                                 Direct Submission.";
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Pred. No. 4.6e
85; Mismatches
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Pred. No. 0.
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Q924S5;
Q1-DEC-2001
01-DEC-2001
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Q1-JUN-2001 (TrEMBLrel. 17, Cr
Q1-JUN-2001 (TrEMBLrel. 18, La
Q1-OCT-2001 (TrEMBLrel. 18, La
HYPOTHETICAL 78.0 KDA PROTEIN.
                                                                                                                                                                                          InterPro; IPR002543; FtsK_SpoIIIE
Pfam; PF01580; FtsK_SpoIIIE; 1.
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
John T.R., Rice J.M., Johnson J.D.;
John T.R., Rice J.M., Johnson J.D.;
"Analysis of pFQ12; a 22.4 kb Frankia
Can. J. Microbiol. 0:0-0(2001).
EMBL; AY027524; AAK20150.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases EMBL; AB064323; BAB62423.1; -. SEQUENCE 950 AA; 105792 MW; D505C3D851B6F0E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                      Hypothetical protein; SEQUENCE 737 AA; 7
                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes;
Actinomycetales; Frank
                                                                                                                                                                                                                                                                                                                                           Frankia sp. CpI1.
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les 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIIHHLDECPHS--QALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSPDGQYVPRIMF 161
-HLSPDGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPAD----TALLLDNMKK 197
                                                                                               LVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSR------GWGDQLIWTQTYEEA 92
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                        ----TINNPLMIGRYRNTQPAEAHLRETYALVVGEQGSGKTNQLYVLTGQLARCTDVIV
                                              LYKSKTSNKPLMIIHHLDECPHSQALKKVFA---ENKEIQKLAEQFVLLNLVYETTDK-- 147
                                                                        LARFSEDLANDADLPAGAGVEV-----LPGTTRRSAVLEISTVDGFAEDLLFGDDYSEL 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MV--EVENVAHEDFQVTEEVKALTAEIVKTIRDIIALNPLYRESVLQMMQAGQRV-----
                                                                                                                        46;
                                                                                                                                  Similarity
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27.5%;
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kineae; Frankiaceae;
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Pred. No. 7.2;
27; Mismatches
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Pred. No. 5.
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01-DEC-2001
01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99206606; pubMed=10192388; Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PREDICTED DISULFIDE BOND ISOMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumo from Japan and CWLO29 from USA."; Nucleic Acids Res. 28:2311-2314(2000). EMBL; AE001673; AAD19071.1; EMBL; AE002251; AAF38711.1; EMBL; AP002548; BAA9311.1; EMBL; AP002548; BAA9311.1; EMBL; AP002548; BAA9314.1; -
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
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25.0%;
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Pred. No.
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sequence update)
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Salzberg S.L.,
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Best Local S
Matches 44
          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Yamamoto K., Cohen F., Sluder A.B.,

"Caenorhabditis elegans nuclear receptor sequences exhibited that the ligand-binding domain fold.";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

-!- SUBLEALUTAR LOCATION: NUCLEAR (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS

FMBL; AF332208; AAK17979.1; -.
                                                                                                                                                                                                                                                                                        Q9BJK8;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
NTCLEAR RECEPTOR NHR-79 (FRAGMENT).
                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O., Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P., Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G., Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H., Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R., Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A., Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 294:849-852(2001).
EMBL; AL596171; CAC97511.1; -.
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STRAIN-CLIP 11262 /
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Charbit A.,
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NCBI_TaxID=1642;
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                                                                                                                                                                                                                          NCBI_TaxID=6239;
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"Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Listeria innocua
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDNMKKALKLLKT
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  IPR000536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berche P., Bloecker H., Brandt P., Chakraborty Chetouani F., Couve E., de Daruvar A., Dehoux
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127525 MW;
Hormone_rec_lig
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1; Mismatches
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Indels

67;

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Length 1151;

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RECEPTORS FAMILY

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the score greater to and is derived
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609.5
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length: 2000000000
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Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231628 seqs, 24425594 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
                                                                                                                                                                                                                      84.6
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Copyright (c) 1993 - 2002 Compugen Ltd
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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            US-08-916-576B-2
US-08-9247-155-106
US-08-9247-155-176B-6
US-08-916-576B-6
US-08-916-576B-6
US-08-916-576B-7
US-08-916-576B-7
US-08-916-576B-7
US-08-926-643-5
US-09-418-540-7
US-09-418-540-7
US-09-418-540-7
US-09-418-540-7
US-09-013-881-5
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US-09-013-881-5
US-09-08-761A-53
US-09-08-761A-53
US-08-921-887-52
US-09-329-749-6
US-08-311-611A-98
US-08-311-611A-98
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(without alignments)
279.537 Million cell updates/sec
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        Sequence 106, App
Sequence 174, App
Sequence 174, App
Sequence 7, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 5, Appli
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Sequence 8, Appli
Sequence 9, Appli
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1 US-08-306-473A-98 1 US-08-261-660A-4 1 US-08-29-762-98 1 US-08-29-762-98 1 US-08-274-303-6 1 US-08-377-91A-2 2 US-08-485-445A-98 2 US-08-779-400-2 2 US-08-95-660-2 3 US-09-119-263-98 4 US-09-919-224-480-98 4 US-09-09-353-98 4 US-09-146-620-2 5 PCT-US94-02455-98 5 PCT-US94-02455-98
US-08-306-473A-98 US-08-261-660A-4 US-08-261-660A-4 US-08-274-39-8 US-08-473-344-98 US-08-274-393-6 US-08-377-3913-6 US-08-485-445A-98 US-08-485-445A-98 US-08-955-660-2 US-08-955-660-2 US-08-955-660-2 US-09-19-263-98 US-09-19-263-98 US-09-19-35-4480-98 US-09-35-4480-98 US-09-35-4480-98 US-09-35-4480-98 US-09-35-4480-98 US-09-35-4480-98 US-09-35-439-98 US-09-35-439-98 US-09-35-439-2 PCT-US94-06931-4

ALIGNMENTS

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RESULT 1
US-08-916-576B-2
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Query Match 84.6
Best Local Similarity 100
Matches 175; Conservative
                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                            TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: MOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
                                                                                      LENGTH: 175 amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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STREET: 1100 NEW
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20005-3934
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                                                                                                                                              175 amino acids
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DILLON, PATRICK J.
EBNER, REINHARD
                 84.6%;
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                                                                                                                                                                                                                                                              1488.0500001
               Score 899; [
Pred. No. 8.
                                      DB 4;
                                Length 175;
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Q

32 MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE 91

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Mismatches

.5e-96; s 0;

Indels

0,

Gaps

0;

1100 NEW

YORK AVENUE, SUITE

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US-08-916-576B-8
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CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-10-04
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                                                                                                                                                        Sequence 8, Application US/08916576B Patent No. 6171816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 175; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
SEQ ID NO 106
LENGTH: 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 106, Application US/09247155A* Patent No. 6312922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                              GENERAL INFORMATION:
APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Complementary DNAs FILE REFERENCE: GENSET.021A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bougueleret, Lydie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dumas Milne Edwards, Jean-Baptiste
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NAME/KEY: SIGNAL
LOCATION: -20...-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                  61 ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
                                                                                                                                                                                                                                                                                                                                                    92 ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP 151
                                                                                                                                                                                                                                                                                                                                                                                                                       32 MEKIPVSAFLLLVALSYTLARDITVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE 91
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STERNE,
                ADDRESS:
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100.0%; Pr
.... 0;
 KESSLER, GOLDSTEIN & FOX, P.L.L.C
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Pred. No. 8.5e-96;
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APPLICANT: DUMAS Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bouqueleret, Lydie
TITLE OF INVESTION: Complementary DNAS
FILE REFERENCE: GENSET.021A
CUBRENT APPLICATION NUMBER: US/09/247,155A
CUBRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-09-247-155-174
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EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PATENT.pm
SEQ ID NO 174
                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 174, Application US/09247155A Patent No. 6312922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 8:
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APPLICATION NUMBER: US 60,
ETILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,68
REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 VPRIMFVDPSLTVRADIXGRYGNRLYAYEPXDXPLLIXNMKKALKLLKTEL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 VPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 AXXSNKPLMVIHHLEDCPYSQALKKVFAENXEIQELAQNFVMLNLVHETTDENLSPDGQY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 LGACLLLVALSXXLA-----XXXKGKDXRPIKGPQTLSRGWGDXIXWVQTYEEGLXK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKTSNKDLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSPDGQY 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WASHINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.3%; Score 609.5; DB 4 71.3%; Pred. No. 1.9e-62; tive 14; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/916,576B
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LENGTH: 131

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US-08-916-576B-6
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Best Local
                                                                                          TELEFAX: (202) 371-25
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: YU, GUO-L
APPLICANT: DILLON, E
APPLICANT: EBDER, RE
APPLICANT: ENDRESS,
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: UNSURE
LOCATION: 40,41,43,60,70,76,82,86,105,107
TNEORMATION: Xaa = any one of the twenty amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SIGNAL LOCATION: -20..-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6
FILING DATE: 23-AUG-1996
                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                        REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 DGQYXP 126
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                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 XLXKSKTSNKPLMIIHHLDXCPHSQALKKXFAENKXIQKLAXQFVXLNLVYETTDKHLSP 120
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                                                                                                                                                                        NAME: STEFFE, ERIC K. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                         CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                        FILING DATE:
                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGQYVP 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
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                                            amino acid
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                                                             166 amino acids
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IVENTION: NOVEL HUMAN GROWTH FACTORS
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             .protein
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                                                                                                            371-2540
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92.9%;
                                                                                                                                                                                                                                           US 60/024,347
                                                                                                                                                                                                                                                                                                                                        Release #1.0,
                                                                                                                                                                                                                                                                                                          US/08/916,576B
                                                                                                                                                                        36,688
                                                                                           6:
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                                                                                                                                                            1488.0500001
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Pred. No. 4.2e-62;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                        Version #1.30
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Best Local Sim
Matches 108;
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GENERAL INFORMATION:
                                                                                                       Query Match
Best Local S
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                                                                                           Matches
                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                          NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE, DOCKET NUMBER: 148
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                    TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 LLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEEALYKSKTSN 100
 90 EEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLA-EQFVLLNLVYETTDKH 148
                                                           39 AFLLLVALSYTLARDTTVKP---GAKKDTKDSRPKLP-----QTLSRGWGDQLIWTQTY 89
                                                                                                                                                                                                    STRANDEDNESS:
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                              SLVCLVLLCSALGEAVLKKPKKQAGTTDTKTDQEPAPIKTKGLKTLDRGWGESIEWVQTY 65
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                                                                                                        Similarity
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                                                                                                                                                                                                                                   183 amino acids
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DILLON, PATRICK
EBNER, REINHARD
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202) 371-2540
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                                                                                                       42.18;
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                                                                                                                                                                                                                                                                                                                             1488.0500001
                                                                                                          Score 448; DB 4;
Pred. No. 8.6e-44;
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                                                                                           Mismatches
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                                                                                                                       Length 183;
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RESULT 8
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Sequence 5, Application US/08884681
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACTION
OPERATING SYSTEM: PC-DOS/MS-
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CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN &
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 172 amino acids
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                                                                                                                 165 SLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLL 202
                                                                                                                                                                    107 HHLDECPHSQALKKVFAENKEIQKLAEQFVLLNL--VYETTDKHLSPDGQYVPRIMFVDP 164
                                                                                                                                                   61 IHKSWCGACKALKPKFAESTEISELSHNFVMVNLEDEEEPKDEDFSPDGGYIPRILFLDP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                2 ETRPRLGATCLLGFSFLLLVISSDGHNGLGKGFGDHIHW-RTLEDGKKEAAASGLPLMVI 60
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                                                                                   SGKVHPEIINENGNPSYKYFYVSAEQVVQGMKEAQERL 158
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EBNER, REINHARD
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                                                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                                                                                Score 222; DB 4; Length 172; Pred. No. 8.8e-18;
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US-09-258-643-5
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; CLONE: 1420920
US-08-884-681-5
                                                Sequence 5, Application US/09258643 Patent No. 6277373 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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CITY: Palo Alto
crate: CA
                APPLICANT:
APPLICANT:
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 APPLICANT:
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                                                                                                                                                                                                            185 PADTALLLDN 194
                                                                                                                                                                                                                                                                                                                  531 FHIGVKVVDE----RRYRKVFEDSVRIMDRMENDFLPSLELSRREFVFENVKFRQLQKGK 586
                                                                                                                                                                                                                                                                                                                                                   107 HHL-----DECPHSQALKKVFAENKEIQKLAE-------QFVLLNLVYETTDK-- 147
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive
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                Hillman, Jennifer L.
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Corley, Neil C.
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Matches
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                                                                                                                                   GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 5:
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TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1420920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF. TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                  APPLICANT: Pot, David A.
APPLICANT: Williams, Lewis T.
APPLICANT: Williams, Lewis T.
APPLICANT: Jefferson, Anne Bennett
APPLICANT: Majerus, Philip W.
TITLE OF INVENTION: No. 6001354el Grb2 Associating Protein and Nucleic
TITLE OF INVENTION: Acids Encoding Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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ADDRESSEE: Incyte Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskett
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity es 45; Conserv
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                                                                                                                                                                                                                                                                                                                           FQISNNGQVPCHFSFIPKLNDSQYCKPWLRAEPFEGYLEPNETV--DIS---
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Pred. No. 1.6;
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                                                                                                                                                                                                                                              Sequence 7, Patent No.
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Best Local
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                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                APPLICANT: Pot, David A.
APPLICANT: Williams, Lewis T.
APPLICANT: Jefferson, Anne Bennett
APPLICANT: Majerus, Philip W.
TITLE OF INVENTION: No. 6296848el Grb2 Associating
TITLE OF INVENTION: Acids Encoding Therefor
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
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APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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LOCATION:
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Local Similarity 23.7%;
es 45; Conservativo
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              CITY: San Francisco
STATE: California
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COUNTRY:
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Pred. No. 1.8;
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                                                 Suite 2000
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US-09-534-638-5
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                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Panula, Pertti A.J.
APPLICANT: Brandt, Annika
APPLICANT: Westerlund, Johanna
TITLE OF INVENTION: Promoter for Neuropeptide FF Promoter and use thereof
TITLE OF INVENTION: for therapy and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 23.7
Matches 45; Conservative
               CURRENT APPLICATION NUMBER: US/09/534,638
CURRENT FILING DATE: 2000-03-27
EARLIER APPLICATION NUMBER: 09/365755
EARLIER FILING DATE: 1999-08-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 129
                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09534638 Patent No. 6320038
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                       FILE REFERENCE: 2530-104
TYPE: PRT
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APPLICATION NUMBER: US 08/560,005
FILING DATE: 17-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: DOW, KAIFER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 TVKPGAKKDTKDSRPK--LPQTLSRGWGDQLIWTQTYEEAL-YKS----KTS-NKPLMII 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1. 968
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 14-003
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COMPUTER: II
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REFERENCE/DOCKET NUMBER: 23
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amino acid
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; TOPOLOGY: linear
; INMEDIATE SOURCE:
; LIBRARY: LUNGNOT
; CLONE: 1376382
US-09-013-881-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Bandman
APPLICANT: Lal, Pr
APPLICANT: Hillman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application Patent No. 613296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                    NAME: BILLINGS, LUCY J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF TELECOMMUNICATION INFORMATION: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Ph
                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gueglo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 3174 POI
CITY: Palo Alto
              25 VRKSRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLI 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: HEREW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 TPVSRLSQSP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 VALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEEALYKSKTSNKPL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 7.3%;
Local Similarity 22.9%;
les 16; Conservative
                                                             Local
                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                            TYPE:
                                                                                                                                                                                                                                                                                       TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                      LENGTH:
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                                          tch 7.3%; Score 78; DB 4; Length 453 al Similarity 22.5%; Pred. No. 1.5; 45; Conservative 34; Mismatches 79; Indels
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                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                        453 amino acids
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3174 Porter Drive
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Hillman, Jennif
Corley, Neil C.
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<del>...</del>
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;; Pred. No. 0.23;
14; Mismatches
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                                               79; Indels
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RESULT 15
US-08-313-185-53
; Sequence 53, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
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PCT-US92-05401-4
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:

NAME: Feit, Irving N.

REGISTRATION NUMBER: 28,601

REFERENCE/DOCKET NUMBER: LEM-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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ADDRESSEE: IMCLONE SYSTEMS INCORPORATED STREET: 180 VARICK STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1160 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                  1000 LGLLSPQAQVEDSRNNLVLRTSSLHLSLTGCRLPK 1034
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                                                                                                                                                                          128 IQKLAEQFVL----LNLVYETTDKHLSPDGQYVPR 158
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                                                                                                                                                                                                                                          68 RPKLPQTLSRGWGDQLIWTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKE 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 19920626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                        Score 78; DB Pred. No. 5.8; Pred. No. 5.8; 17; Mismatches
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Search completed: October Job time: 19 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amallo
APPLICANT: Bodimer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                  145
                                                                                                                                                                                                                                                                                                                211 GPNHS-PLSAAAAIRTFRMGMNDEETVA---LIAGGHTLGKTHGAGPASHVGPPEAAPIE 266
                                                                              379 THRDMGPKRYIGPEVPKEDLIWQDPPQYPTEDIILKAAIAASGLVSELVSAWASAST 435
                                                                                                                                                       325 APDIIPDPFDPSKKRKPTMLYTDLLRFDPEYEKISRRFLNDPEFEAFARAW-----FKL 378
                                                                                                                                                                                                                                   267 AQGL--GWASSYGSGVGADAITSGEVVWTQTPTQWNFFENLFYEWVLTKSPAGAQEAVDG 324
                                                                                                                                                                                             97
                                                                                                                                                                                                                                                                                                                                                12 GPHPSRRLTQGRWVRKSRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Finnegan, Henderson, ADDRESSEE: Dunner STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                          72 PQTLSRGWGD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
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                                                                                                                TDKHLSPD----GQYVPR--IMFVDPSLTVRADI-----TGRYSNRLYAYEPADT 188
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Zhang, Ying
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                              score greater tand is derived
                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                 Score
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                                                                                                                                                                                                                       Query
Match
                                                                                                                                                                                                                                                                                                                            is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              October 9, 2002, 16:40:27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989 DAT: *
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990 DAT: *
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SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
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AAY76590
AAG75621
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Breast cancer cell
Human huXAG-1/CCSG
Human secreted pro
                                     Human PRO1030 prot
Breast cancer cell
                                                                           Human protein comp
Secreted protein 1
                                                                                                              zsig10 polypeptide
Human XAG growth f
                                                                                                                                                    Human prostate tum
Human ovarian tumo
Human colon cancer
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3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.9	3.9	4.4	4.4	4.9	4.9	4.9	5.3	ნ. ა	υ		6.8	8.3	11.7	11.7	11.7	11.7	11.7	11.7	11.7	14.1	20.4	26.7	•	•	56.3
119	109	109	109	105	105	73	10	1284	315	9	9	180	70	11	11	11	1	11	39	56	168	166	166	166	166	166	166	89	62	56	131	115	116
22	22	22	21	22	22	22	22	22	22	22	22	22	20	22	22	22	22	22	21	20	22	22	22	22	22	21	19	20	20	20	20	21	20
ААМ25807	AAB80983	AAM40426	AAG03933	AAO04178	AAM91788	AAM86554	AAM43189	ABB61690	AAG73015	AAU07648	AAU25812	AAG73737	AAY11654	AAU25806	AAU25805	AAU25804	AAU08806	AAU08805	AAB58921	AAY11939	AAM24502	AAU07647	AAB31192	AAB72205	AAU25728	AAB00194	AAW37846	AAY76568	AAY11882	AAY11881	AAY59718	AAY64672	AAY12312
Human protein sequ	Human hARE-RBP1.	Human polypeptide	Human secreted pro	Human polypeptide	Human immune/haema	Human immune/haema	Mycoplasma genital	Drosophila melanog	Olfactory receptor	Human BCMP 11 pept	Breast cancer-asso	Human colon cancer	Ų,			cancer-	cancer		~	5' EST	tumour 1	BCMP		<u> </u>	t cancer-	4	XAG grow	Human ovarian tumo	5' EST	5' EST	d prot	5' EST rel	Human 5' EST secre

ALIGNMENTS

RESULT 1
AAY73837
ID AAY7

AAY73837 standard; Protein;

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AAY73837;

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Claim 23; Page 318; 502pp; German.
                                          WPI; 1999-621386/54.
N-PSDB; AAZ52865.
                                                                                                                                                                                                                 Human prostate tumor EST fragment derived protein #24
                                                                                                                                                                                                                                  14-MAR-2000
                 proteins
                        New human nucleic acid sequences from pancreatic tumors, and related
                                                                                                                      28-APR-1998;
                                                                                                                                       04-NOV-1999
                                                                                                                                                        DE19820190-A1:
                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                         treatment.
                                                                                                                                                                                                Pancreas; tumor; EST; expressed sequence tag; human; cytostatic;
                                                                   Rosenthal A, Specht T,
                                                                                    (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                                                                      28-APR-1998;
                                                                                                                                                                                                                                 (first entry)
                                                                                                      98DE-1020190
                                                                                                                      98DE-1020190
                                                                    Hinzmann
                                                                    В,
                                                                    Schmitt
                                                                    Α,
                                                                    Pilarsky
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RESULT 2
AAY76590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel polypeptides and their encoding nucleic acids derived from human pancreatic tumor tissue which have cytostatic activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. AAY73814-Y74252 represent protein fragments encoded by the human pancreatic tumor cDNA library derived expressed sequence tag (EST) sequences represented in AAZ52858-Z53014.
           This invention describes novel nucleic acid (cDNA) sequences (A) which have anticancer activity and are highly expressed in ovarian tumor tissue (and some also in testis and breast cancer tissue). The products of the invention can be used for gene therapy (A) are used (1) for
                                                                                             New nucleic acid sequences expressed in ovarian, tissues, and derived polypeptides, for treatment identification of therapeutic agents
                                                                                                                                                        WPI; 1999-591920/51.
                                                                                                                                                                               Rosenthal A,
                                                                                                                                                                                                                              09-APR-1998;
                                                                                                                                                                                                                                                    09-APR-1998;
                                                                                                                                                                                                                                                                                                    DE19817557-A1
                                                                                                                                                                                                                                                                                                                                                            Expressed sequence tag; EST;
                                                                                                                                                                                                                                                                                                                                                                                  Human ovarian tumor EST fragment encoded protein
                                                                                                                                                                                                                                                                                                                                                                                                           10-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY76590 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                      (META-) METAGEN GES GENOMFORSCHUNG MBH
                                                                                                                                                                                                                                                                            21-OCT-1999
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                                                                      Page 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 AA;
 expression of
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                                                                                                                                                                                Specht
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                                                                                                                                                                                Hinzmann
polypeptides
                                                                        German.
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                                                                                                                                                                                                                                                                                                                                                            human;
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                                                                                                                                                                               В,
                                                                                                                                                                                                                                                                                                                                                             ovarian tumor; anticancer;
                                                                                                                                                                                Schmitt
 (B)
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                                                                                                         ovarian cancer
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                                                                                                                                                                                Dahl
                                                                                                         cancer
er and
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RESULT 3
AAG75621
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes. (B) are used (i) to identify agents suitable for treatment of ovarian cancer; (ii) directly for treating this form of cancer (including expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling ESTs (expressed sequence tags) from a particular tissue type before comparison of the expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTs from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. ANY76505-Y76508 represent protein fragments encoded by the human ovarian tumor cDNA library derived EST fragments represented in AAZ77450-Z77572.
                                                                                                                                                                      29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                    05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                      03-SEP-2001
                                               Nucleic acids encoding 4277 human useful for preventing, diagnosing
                                                                                                                        Ruben SM,
                                                                                                                                               (HUMA-) HUMAN GENOME
                                                                                                                                                                                                         28-SEP-2000; 2000WO-US26524
                                                                                                                                                                                                                                                           WO200122920-A2
                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                          colorectal carcinoma
                                                                                                                                                                                                                                                                                                                       Human; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                               AAG75621;
                                                                                                                                                                                                                                                                                                                                                                                                                   AAG75621 standard; Protein;
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                                                                                                                                                                                                                                                                                  sapiens
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                                                                                                                                                                                                                                                                                                                                              colon
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                                                                                                                        Barash SC,
                                                                                                                                                                                                                                                                                                                                            cancer antigen
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99US-0163280.
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100.0%;
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                                                                                                                                                                                                                                                                                                                       cancer antigen;
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Pred. No.
                                                                                                                        CE,
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                                                colon cancer-associated polypeptides,
and/or treating colorectal cancers -
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2.9e-182;
                                                                                                                                                                                                                                                                                                                       diagnosis;
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                                                                                                                                                                                                                                                                                                                        detection;
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AAH32943 to AAH37195 and

AAG73514 9803pp;

to AAG77788 English

represent

human colon

Claim 11;

Page 7865-7866;

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AAW77365
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps. by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and AAB77789 represent sequences used in the exemplification of the
WPI; 1998-531566/45.
N-PSDB; AAV59320.
                                                          Sheppard
                                                                                                                                                                                                                                                                     WO9841627-A1
                                                                                                                                                                                                                                                                                                                                              Human; mucous-mediated function; adhesion; tumour metastasis; bacterial colonisation; microbial infection; AIDS; cystic fibrosis; chronic obstructive pulmonary disease; asthma; Crohn's disease; sinonasal inflammatory disease; inflammatory bowel disease; bronchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                        zsig10 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW77365 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention.
                                                                                                                                            19-MAR-1997;
                                                                                                                                                                                   18-MAR-1998;
                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .B. Pages 666 to 682 and page 7053 of the sequence listing were issing at time of publication, meaning no sequences are present EQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQFVLLNLVYETTDKHLSPDGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QTLSRGWGDQLIWTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHPSRRLTQGRWVRKSRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNMKKALKLLKTEL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QTLSRGWGDQLIWTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHPSRRLTQGRWVRKSRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQFVLLNLVYETTDKHLSPDGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLL
                                                                                                   ) ZYMOGENETICS
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                                                            РО
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                          97US-0039631
                                                                                                                                                                                   98WO-US05251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein; 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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Peptide

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RESULT 5
AAW37844
ID AAW37844
ID AAW37844
ID AAW3784
AC AAW3
AC AAW3
AC AAW3
AC Huma
XX Huxa
AKW breaa
KW breaa
KW breaa
KW wour
CXX Homc
XX Homc
YY Pept
FT Pept
FT Pep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The human polypeptide zsigl0 is involved in mucous-mediated functions such as adhesion. The products of the invention can be used in the stunned treatment of e.g. tumour metastasis, bacterial colonisation, susceptibility to and persistence of infection, microbial infections, AIDS, cystic fibrosis, chronic obstructive pulmonary disease, asthma, sinonasal inflammatory disease, inflammatory bowel disease, bronchitis, or Crohn's disease. The products can also be used for detection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated mucous-associated polypeptide, zsig10 - used to develop products for treating e.g. tumour metastasis, microbial infections, cystic fibrosis, asthma, bronchitis or inflammatory bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                                          HUXAG-1; XAG; growth factor; colon cancer; tumour marker;
breast disease; liver disease; lung disease; emphysema;
wound healing; diagnosis; therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW37844 standard; Protein; 175
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                                                   Peptide
                                                                                                    Peptide
                                                                                                                                                  Peptide
                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human XAG growth factor huXAG-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175
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                                                                                                                                                     /note=
61..72
/label= Epitope
/note= "Claim 12"
138..150
                                                 /label= Epitope
/note= "Claim 12"
113..125
                                                                                                                  /label= Epitope
/note= "Claim 12"
                                                                                                                                                                                                                                      /label= Epitope
                                                                                                                                                                                                                                                                      /label= Mat_protein
/note= "Claim 11"
                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                       /label= Epitope
                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                       /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             screening.
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                                                                                                                                                                   "Claim
                                                                                                                                                                                                                     "Claim 12"

    Mismatches

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Pred. No. 1.2e-163;
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                                                                                                                                                                                                                                                                                                                                                                                                     of hepatocytes to alleviate or treat liver diseases and pathologies such as fulminant liver failure caused by cirrhosis, liver damage caused by viral hepatitis and toxic substances. They can also be used to stimulate or promote liver regeneration, e.g. after surgery. They can also be used to prevent and heal damage to the lungs caused by various pathological states. They can be used to stimulate proliferation and differentiation and promote the repair of alveoli and bronchiolar epithelium to prevent, attenuate, or treat acute or chronic lung damage, e.g. emphysema, which results in the progressive loss of alveoli, and inhalation injuries, e.g. resulting from smoke inhalation and burns, that cause necrosis of the bronchiolar epithelium and alveoli. They can also be used to stimulate the proliferation and differentiation of breast tissue and could therefore be used to promote healing of breast tissue
                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                Matches 175;
                                                                                                                                                                                                                                                                                                                injury due to surgery, trauma or cancer. Antagonists can to treat hyperproliferative disorders, including cancer. particular hepatocellular carcinoma, osteoclastoma, breas or colon cancer. The products can also be used for detections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human growth factors also including huXAG-2 (see AAW37845) and huXAG-3 (see AAW37846). These proteins share homology with the XAG protein of xanopus laevis, which is involved in embryogenesis and is expressed in adult tissue. huXAG-1 is specifically found in cancerous colon cells and may therefore be a growth factor for colon cancer. huXAG-1 cDNA (see AAV19125) was isolated from a cDNA library derived from human colon cancer tissue. Vectors, host cells, antibodies, and screening methods for identifying agonists and antagonists of huXAG-1 are provided. HuXAG polypeptides are growth factors and can be used to stimulate proliferation of cells. They can be used to stimulate the proliferation as and methologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated human XAG growth factor(s) - used to develop for treating e.g. liver, lung or breast diseases or hyperproliferative disorders, e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1; 141pp; English.
                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This polypeptide comprises huXAG-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-169093/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-1998.
121
                                                                      61
                                                                                                     92
                                                                                                                                          Local Similarity
                                                                ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP 151
DGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV19155
                                                                                                                                                                                                                                                                                    175 AA
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                                                                                                                                                                                                                Conservative
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/note= "Claim 12"
                                                                                                                                                                                                                                85.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCI INC
                                                                                                                                                                                                                                                                                                                                      products can also be used for detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endress
                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                Score 175; DB 19;
Pred. No. 1.2e-163;
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                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a member of a novel family huXAG-2 (see AAW37845) and
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                                                                                                                                                                                                                                                                                                                                                                                           Antagonists can
                                                                                                                                                                                                                                               Length 175;
                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                          breast cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           products
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 175
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RESULT 6
AAW37872
RESULT 7
AAY59675
ID AAY59675 standard; Protein; 175
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                                                                                                                                                                                                   Matches
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Best Local
                                                                                                                                                                                                                                                                 This is the amino acid sequence of a novel human protein comprising a secretory signal isolated from stomach cancer cells. Its proteins can be used as nutritional sources or supplements. The proteins may also have cytokine functions, immune modulating functions, haematopoiesis regulating activity, activiny/inhibin regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein; secretory signal; nutritional source; immunity; haematopoiesis; activin; inhibin; tumour; c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW37872 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                         Human proteins with secretory signal sequences - used to treat immune deficiencies, infections, tumours, and haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-207380/18.
N-PSDB; AAV29047, AAV29048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stomach cancer cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chemokinetic; thrombolytic; anti-inflammatory; inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Pages 79; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kato S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PROT-) PROTEGENE INC.
(SAGA) SAGAMI CHEM RES CENTRE.
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                                                                                                                                                                                                                                               Sequence
                                                           121
                                                                                 152
                                                                                                         61
                                                                                                                                                                  L
                                                          MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE
                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kobayashi M, Sekine S,
                                                                                                                                                                                                                                                                                                                                                                                                etc.
                                                                                                                                                                                                                                               175 AA;
                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96JP-0243060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-JP03239
                                                                                                                                                                                                             85.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    secretory signal amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175
                                                                                                                                                                                                               Score 175; pred. No.
                                                                                                                                                                                                   0;
                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamaguchi
                                                                                                                                                                                                             DB 19; 1
. 1.2e-163;
                                                                                                                                                                                                                        Length 175;
                                                                                                                                                                                                    Indels
                                                                                                                                                                                                    0;
                                                                                                                                                                                                   Gaps
                                                                                                                                                         60
                                                                                                                                                                             91
                                                                                                           120
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CC This sequence represents a human secreted protein of the invention.

CC The extended cDNAs (or genomic DNAs obtainable from them) may be used to CC prepare PCR primers and probes. These are useful for forensic matching or CC positive identification by DNA sequencing. They may also be used in CC alternative fingerprint identification techniques. Antibodies against the CC proteins encoded by the extended cDNAs are useful in identification of CC tissue types or cell species, as well as identifying tissue specific CC soluble proteins. The sequences can be used for chromosome mapping and CC identification of genes associated with hereditary diseases or drug CC response. Signal sequences from the cDNAs can be used in construction of CC secretion vectors. Other sequences derived from the extended cDNAs can be used to clone upstream genomic DNA sequences including promoters. This is in turn useful for identifying proteins that interact with promoter CC sequences. Some of the proteins may be useful in diagnosing and treating CC cardiovascular and neurodegenerative disorders, autoimmune diseases, and CC rheumatic diseases, embryogenic disorders, hypertension, renal injury, amino acidurias, hypoglycaemia, male rat infertility and myopathies.
                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-FEB-1998;
13-APR-1998;
10-AUG-1998;
04-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome mapping; human; hereditary disease; diagnosis; cancer; hyperlipidaemia; cardiovascular; neurodegenerative disorder; therapy; autoimmune disease; rheumatic disease; embryogenic disorder; myopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Extended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEST )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-AUG-1999
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                                                                                                                                                                       MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens
DGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL
                                                                        ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
                                                                                                                                                MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE
                                                 ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Page 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           injury; amino aciduria; hypoglycaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ40803
                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNAs useful for
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                                                                                                                                                                                                                                                                                                                                                  175
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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98US-0081563.
98US-0096116.
98US-0099273.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108-008-5-0-A6-FL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244pp;
                                                                                                                                                                                                                                                                    85.0%;
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                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                    Score 175; DB 20;
Pred. No. 1.2e-163;
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                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                            Length 175;
                                                                                                                                                                                                                                                Indels
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RESULT 8
AAB24070
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PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1132, PRO1182, PRO1184, PRO1281, PRO1281, PRO2198, PRO339, PRO834, PRO1317, PRO1170, PRO2094, PRO2145 OR PRO2198, PRO antagonists can be used to inhibit tumour cell growth. The PRO polypeptides and nucleotides are useful in the treatment, diagnosis and prevention of cancer. The antibodies and other cantinoses characterised by overexpression and/or activation of the amplified PRO genes. Exemplary conditions or disorders to be treated with such cantibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukaemias and lymphoid malignancies, other disorders such as neuronal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR primers and hybridisation probes used in the isolation of the human PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-1999;
02-JUN-1999;
03-JUN-1999;
23-JUL-1999;
07-JUL-1999;
26-JUL-1999;
30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ashkenazi AJ,
Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; tumour; diagnosis; neoplastic disease; neoplastic cell growt proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antinflammatory; immunosuppressive; immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; anglogenic; hypothalamic disorder; plandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; epithelial disorder; stromal disorder; blastocoelic disorder;
                                                                                                                                                                                                                                                                         one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009
                                                                                                                                                                                                                                                                                           The present invention describes an isolated antibody one of the human PRO proteins designated PRO212, PRO
                                                                                                                                                                                                                                                                                                                                                                       Thirty PRO polynucleotides encoding treatment, diagnosis and prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-DEC-1999;
05-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAC58380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammatory disorder;
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99US-0141037.
99US-0143048.
99US-0145698.
99WO-US28313.
99WO-US28313.
99WO-US30911.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wood
                                                                                                                                                                                                                                                                                                                                          28; 286pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US05028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,
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                                                                                                                                                                                                                                                                                                                                                                                      PRO polypeptides,
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                                                                                                                                                                                                                                                                                                                                                                         cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neoplastic cell growth;
cancer; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillan KJ,
                                                                                                                                                                                                                                                                                                          that binds
                                                                                                                                                                                                                                                                                                                                                                                          useful
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RESULT 9
AAU08804
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
         The invention describes the novel use of a protein found in breast cancer cell membranes (BCMP 7) for diagnosing, preventing and treating breast cancers. The peptide has cytostatic action and potential uses in gene therapy and in vaccines. The polypeptide, antisense nucleic acids or fusion proteins comprising and Green Fluorescent protein or the DsRc Fluorescent protein, antibodies specific for and/or nucleic acid are used for the prevention and/or treatment of breast cancer. Antibodies
                                                                                                                              Diagnosing, preventing cell membrane protein !
                                                                                                                                                                                                                                                                                                                                                                        Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences. AAC58367 to PRO polynucleotide and the present invention.
                                                                                                       Claim
                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                 Boyd RS,
                                                                                                                                                                                                                                                                                           30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Breast cancer cell membrane protein 7; BCMP 7; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU08804 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                        (OXFO-)
                                                                                                                                                                                                                                              25-FEB-2000;
                                                                                                                                                                                                                                                                    21-FEB-2001;
                                                                                                                                                                                                                                                                                                                  WO200163290-A1
                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                              metastasis;
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                                                                                                                                                              2001-570651/64.
DB; AAS13480.
                                                                                                                                                                                                                                                                                                                                                                                                            sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEKTPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
                                                                                                      1;
                                                                                                                                                                                                                       OXFORD GLYCOSCIENCES UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                      Fig 1; 62pp; English.
                                                                                                                                                                                                Stamps AC,
                                                                                                                                                                                                                                                                                                                                                                                                                                  7p21.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic;
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                                                                                                                                                                                                                                                                    2001WO-GB00734
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                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell membrane associated
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21..175
                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         note-
                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                    175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.0%;
                                                                                                                             g and treating
BCMP 7 -
                                                                                                                                                                                                Terrett JA,
                                                                                                                                                                                                                                                                                                                                                             "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC58396 and AAB24057 to AAB24089 represent human protein sequences given in the exemplification of
                                                                                                                                                                                                                                                                                                                                     "Mature BCMP 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
for
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screening
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy; antibody;
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                                                                                                                                       breast cancer using
for and/or diagnosis
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. 1.2e-163;
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Best Local S
Matches 175
This invention relates to a human growth factor polypeptide huXAG-1 also known as a colon cancer specific gene (CCSG). HuXAG-1 stimulates cell proliferation as a growth factor. The HuXAG-1 protein is useful for identifying compounds capable of enhancing or inhibiting cellular response induced by huXAG-1. The protein is also useful for stimulating proliferation of cells e.g. colon, breast, liver and lung cells, and hepatocytes. It is useful for alleviating or treating liver diseases and pathologies such as fulminant liver failure caused by cirrhosis, liver damage caused by viral hepatitis and toxic substances, for preventing and treating damage to the lungs caused by various pathological states and for promoting healing of breast tissue injury due to surgery, trauma or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer in a patient. The method for monitoring/assessing breast treatment in a patient and for the identification of metastatic, cancer cells in samples from a patient. This sequence is breast cancer cell associated protein 7 (BCMP 7), encoded by a gene loc chromosome 7p21.3, described in the method of the invention.
                                                                                                                                                                                     Claim 165; Fig 1;
                                                                                                                                                                                                                  Novel human growth factor polypeptide useful for diagnosing an treating colon cancer and liver diseases, to prevent and heal the lungs and for identifying modulators of therapeutic use -
                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                            WPI;
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DB; AAF63314.
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RESULT 11
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Best Local S
Matches 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer. HuXAG-1 and the identified antagonist are useful for treating cancer, in particular colon cancer. Detecting altered levels of huXAG- and its polynucleotides are useful for diagnosing or detecting cancer mammals. The gene encoding huXAG-1 is useful for monitoring human colorectal carcinoma. huXAG-1 nucleic acid molecules are also useful fermionsome identification. The present sequence represents the huXAG-1
          The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' and and the first being the first markets with intact 5' and and the first being the first markets with intact 5' and and the first markets with intact 5'.
                                                                                                                                                                                                      New nucleic acid that is a 5' expressed sequence tag (5' EST) is obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and diagnostic, forensic, gene therapy and chromosome mapping processors.
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used to
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Pred. No.
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1.2e-163;
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Best Local
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                                        AAX41094 to AAX41347 represent 5' expressed sequence tags (ESTs) for human secreted proteins, and encode the proteins given in AAX12261 to AAX12514, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation;
                                                                                                                                                                                           New nucleic acids encoding human secreted proteins - obtained cDNA libraries prepared from e.g. liver, ovary, brain, prostatkidney, lung, umbilical cord, placenta and colon tissue
                                                                                                                                                                                                                                                                                                                                                                01-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                  Claim
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               activity,
                             proliferation/differentiation activity, haematopoiesis regulating
                                                                                                                                                                                                                                                                                                                               (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reproductive hormone regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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DB; AAX41145.
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tissue growth regulating activity, reproductive g activity, chemotactic/ chemokinetic activity, l
                                                                                                                                                               Page 682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-inflammatory; tumour inhibition.
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100.0%;
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Pred. No. 1.2e-115;
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                                                                                                                                                                                                                                                                                                    Lacroix
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 haemostatic
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RESULT 13
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Best Local S
Matches 116
       sequences, corresponding to human secreted proteins. AAY64651 to AAY6448 represent the EST-related proteins corresponding to AAZ42265 AAZ43052. The 5' ESTs can be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated regions (UTRs) and upstream regulatory regions which control the location, development stage, rate, and quantity of protein synthesis, well as stability of mRNA. The ESTs are also useful as probes for chromosome mapping, and to obtain full length cDNA clones. The ESTs calso be used in forensic procedures to identify individuals, or in diagnostic procedures to identify individuals having genetic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombolytic activity, receptor/ ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell.
                                                                                                                                                                                                                                                              WPI; 2000-038446/03
N-PSDB; AAZ42286.
                                                                                                                                                          AAZ42265 to AAZ43075 represent novel 5' expressed sequence
                                                                                                                                                                                                                     diagnostic,
                                                                                                                                                                                                                                                                                                                                                                  09-APR-1998;
28-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regulation; identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     jene therapy; chromosome mapping
forensic; location; development;
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                                                                                                                                                                                                               secreted protein 5' expressed ostic, forensic, gene therapy,
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116; Conserv
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                                                                                                                                                                                     Page 604; 837pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; expressed sequence tag; secreted protein; diagnosis;
chromosome mapping; upstream regulatory sequence;
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98US-0069047
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                                                                                                                                                                                                                                                                                                        Duclert
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Pred. No.
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synthesis; stability;
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also
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Best Local :
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13-APR-1998;
10-AUG-1998;
This sequence represents a human secreted protein of the invention. The extended cDNAs (or genomic DNAs obtainable from them) may be used to prepare PCR primers and probes. These are useful for forensic matching or positive identification by DNA sequencing. They may also be used in alternative fingerprint identification techniques. Antibodies against the proteins encoded by the extended cDNAs are useful in identification of tissue types or cell species, as well as identifying tissue specific
                                                                                                                                                Extended specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy protocols. The nucleic acids encoding signal peptides used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypepti into a cell. The proteins encoded by the EST sequences may be useful treating a variety of human conditions. Secreted proteins have therapeutic value, and the identification of new secreted proteins valuable. AAX42249 to AAX42264 and AAX64644 to AAX64650 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome mapping; human; hereditary disease; diagnosis; cancer; hyperlipidaemia; cardiovascular; neurodegenerative disorder; therapy; autoimmune disease; rheumatic disease; embryogenic disorder; myopathy; renal injury; amino aciduria; hypoglycaemia; male rat infertility;
                                                                                                                                                                                              N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                        09-FEB-1999;
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                                                                                                                                                cDNAs useful
antibodies -
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                                                                                                                    Page
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98US-0081563.
98US-0096116.
98US-0099273.
                                                                                                                    240;
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                                                                                                                   244pp; English
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Pred. No.
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ay be useful in
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RESULT 15
AAY11881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; prostate; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
                                                                                                                                                 AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTs) for human secreted proteins expressed in prostate, and encode the proteins given in AAX11716 to AAX11993 respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene
                            products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation and differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, reproductive hormone
                                                                                                                                                                                                                                                                                                                                        Claim 34; Page 603; 675pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              New isolated prostate-derived nucleic acids - used to develop products which may have cytokine, immune regulatory, haematop regulating, anti-inflammatory or tumour inhibition activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duclert A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY11881;
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regulating activity, chemotactic/chemokinetic activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET
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59; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX40603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dumas Milne
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haemostatic and

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Best Local
                                                                                                                                                                    thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptides can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell.
                                                                                                                                       Sequence
              32 MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWT
_
MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWT
                                                                                    Similarity
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                                                                 Conservative
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100.0%;
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Pred. No.
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2.6e-46;
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Perfect score:
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Copyright (c) 1993 - 2002 Compugen Ltd
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T34016	S18158	S22621	B85358	T34412	AE1952	JC5674	PD0007	JC5150	JC5151	н82339	T22810	S53965	S15809	AG0386	S47006
hypothetical prote	lipoprotein lipase	phosphomannomutase	SERINE CARBOXYPEPT	hypothetical prote	hypothetical prote	cytochrome P450 no	cytochrome P450 no	nitric-oxide reduc	nitric-oxide reduc	conserved hypothet	hypothetical prote	hypothetical prote	cytochrome P450 CY	5-amino-6-(5-phosp	zinc finger protei

ALIGNMENTS

RESULT 1 JE0350

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C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 26-Aug-1999
C;Accession: JC5201; Pc4303
R;Thomas, M.B.; Haines, S.L.; Akeson, R.A.
Gene 178, 1-5, 1996
A;Title: Chemoreceptors expressed in taste, olfactory and male reproductive A;Reference number: JC5200; MUID:97080538
A;Accession: JC5201
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JC5201
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Biochem. Biophys. Res. Commun. 251, 111-116, 1998
A;Title: hAG-2, the human homologue of the Xenopus laevis
A;Reference number: JE0350; MUID:99009231
A;Accession: JE0350
                                     A; Molecule type: DNA
A; Residues: 1-315 < THO1>
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A; Cross-references: A; Accession: PC4303
                                                                                                                                                                                                                                                           chemoreceptor TB567 - rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Comment: This protein is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AF007791; NID:g3779196; PIDN:AAC77358.1; PID:g3779197 C;Comment: This protein is coexpressed with estrogen receptor (ER) in breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-175 < THO>
                                                                          A; Status: preliminary; nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ilarity 100.0%;
Conservative (
                  GB:U50948; NID:g1256390; PIDN:AAC52910.1; PID:g1256391
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; Pred. No. 9.4e-168;
                                                                             sequence
                                                                                                                                         olfactory and male reproductive tissues
                                                                               not shown
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A; Residues: 144-151; 270-
A; Experimental source: t
C; Comment: This protein
C; Genetics:
A; Gene: tb567
C; Superfamily: olfactory
C; Keywords: olfaction; t
F; 88-79/Domain: transmem
F; 101-120/Domain: transmem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Notacus rooms A; Acades type: DNA
A; Residues: 1-637 < WHI>
A; Cross references: GB: AE001863;
A; Cross references: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable acyl-CoA dehydrogenase - Deinococcus radiodurans (strain C;SpecLes: Deinococcus radiodurans C;Date: 03-Dec:1999 #sequence_revision 03-Dec:1999 #text_change 31 C;Accession: C75578 # R;White, O.; Eisen, J. Heidelberg, J.F.; Hickey, E.K.; Peterson M; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                     hypothetical protein APE2531 - Aeropyrum pernix (strain K1) C;Species: Aeropyrum pernix C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_ch C;Accession: C72486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
The B; Conserv
                                                                       A; Reference number: A72450; A; Accession: C72486
                                                                                        A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy A;Reference number: A72450; MUID:99310339
                                                                                                                                                R;Kawarabayasi, Y.; Hino, Y.; awa, H.; Takamiya, M.; Masuda
                                                                                                                                                                                                                                                                                                                                        B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S.; Smith, H.O.; Venter, J.C
Science 286, 1571-1577, 1999
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                                                                                                                           DNA Res. 6, 83-101, 1999
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                                                      Status: preliminary
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-49/Domain: transmembrane #status predicted <TM1>58-79/Domain: transmembrane #status predicted <TM2>
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Residues: 144-151;270-277 <THO2>
Experimental source: taste bud
Comment: This protein is coupled
                     Residues:
                                  Molecule type: DNA
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references:
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                   1-101 <KAW>
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8; Conser
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 DDBJ:AP000064; NID:g5105945; PIDN:BAA81547.1;
                                                                                                                                                Masuda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            taste bud; transmembrane
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                                                                                                                                                Horikawa, H.; Y., S.; Funahashi,
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                                                                                                                                                                  H.; Yamazaki,
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Tanaka, T.; Kudoh, Y.;
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, L.; Utterback, T.; Zalewski,
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C.; Ma
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A; Accession: A03163
A; Accession: type: protein
A; Molecule type: protein
A; Residues: 23-108 <STE>
                                                                                                                                                                                             C;Superfamily: colipase
C;Keywords: lipid digestlon; lipid hydrolysis; pancreas
C;Keywords: lipid digestlon; lipid hydrolysis; pancreas
E;117/Domain: signal sequence #status predicted <SIG>
E;18-22/Domain: amino-terminal propeptide #status predicted <APP>
E;18-22/Domain: amino-terminal propeptide #status predicted <CPP>
E;23-108/Product: colipase #status experimental <AAT>
E;109-112/Domain: carboxyl-terminal propeptide #status predicted
E;34-104,40-56,44-80,45-78,66-86/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross references: GB:J02883; NID:g180885; PIDN:AAA52054.1; PID:g180886 A;Note: evidence of partial N-glycosylation, possibly at Asn-43 R;Sternby, B.; Engstrom, A.; Hellman, U.; Vihert, A.M.; Sternby, N.H.; Bc Biochim. Biophys. Acta 784, 75-80, 1984 Biochim. Biophys. Acta 784, 75-80, 1984 A;Title: The primary sequence of human pancreatic colipase. A;Reference number: A90652; MUID:84104937
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R;Sims, H.F.; Lowe, M.E.
Biochemistry 31, 7120-7125, 1992
A;Title: The human colipase gene: isolation, chromosomal location, A;Reference number: A42568; MUID:92353041
A;Accession: A42568
                                                                                                                                                                                                                                                                                                                                                     A;Gene: GDB:CLPS
A;Cross-references: GDB:127277; OMIM:120105
A;Map position: 6pter-6p21.1
A;Introns: 28/3; 69/3
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A;Title: Cloning and characterization of the human colipase cDNA
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A; Residues: 1-112 <LOW>
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C;Date: 04-Dec-1986 #sequence_revision 19-May-1995 #text_change 08-Dec-2000
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A;Note: sequence extracted from NCBI backbone (NCBIN:110576, NCBIN:110578,
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A; Residues: 1-112 <SIM>
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R; Hayashi, T.; Makino, K.; Ohnishi, M. gasawara, N.; Yasunaga, T.; Kuhara, S. DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of 6 A; Title: Complete genome sequence of 6 A; Reference number: A99629; MUID:21155 A; Accession: E99903
A; Status: preliminary
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DNA Res. 8, 11-22, 2001
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence
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C;Date: 18-Jul-2001 #sequence_revision 18-
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C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: B95024
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson
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A; Residues: 1-114 <HAY>
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A; Residues: 1-112 < KUR>
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A;Accession: B95024
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  A; Molecule
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type: DNA
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29; MUID:21156231; PMID:11258796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 7;
Pred. No.
                                                                                                                                                                     S ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kurokawa, K.; Ishii, K.;
Shiba, T.; Hattori, M.;
                                                                                                                                                                     Kurokawa, K.;
Shiba, T.; Hat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli (strain 0157:H7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
28;
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                                                                                                                                                                     Hattori,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                Ishii, K.;
                                                                                                                                                                                                                                                                                                             coli (strain 0157:H7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli 0157:H7
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M.R.; Radune,
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                                                                                                                                                                  Shinagawa,
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Shinagawa, H.
                                                                                                                                                                     Yokoyama, K.;
Shinagawa, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSPDB:GN00164;
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                                                                                                             coli
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e, D.; Holtzapple,
                                                                                                                O157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B.A.; Morri pneumoniae.
                                                                                                                                                                                                                                                                                                                substrain
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A; Cross-references: GB:BK
A; Cross-references: st
C; Genetics:
A; Gene: ECs2197
C; Superfamily: hypothetic
                                                                                                                                                                                          A; Experimental s
C; Genetics:
A; Gene: Z2099
C; Superfamily: h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown protein encoded within prophage CP-9330 [imported] - Escherichia colicySpecies: Escherichia colicySpecies: Escherichia colicyDate: 16:Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: E85713 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: E85713 #sequence_revision 16-Feb-2001 #sequence_re
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E85713
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C;Superfamily:
                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-14 <STO>
A;Cross-references: GB:AE005174; NID:g12515051; E
A;Experimental source: strain 0157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: C; Genetics:
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R;Perna, N.T.; Plunkett III, G.; Burland, V.;
iller, L., Grotbeck, E.J.; Davis, N.W.; Lim, I
Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein Z1498 [imported] - Escherichia coli (strain O157:H7, s
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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A; Residues: 1-114 <STO>
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                       KALKLLK
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7; Conser
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ilarity 100.0%;
Conservative
                                                                            3.4%; Score 7; llarity 100.0%; Pred. No. Conservative 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        A85480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     of enterohemorrhagic Escherichia 30; MUID:21074935; PMID:11206551
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                                                                               Pred. No. 28;
Mismatches
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28;
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A.; Dimalanta,
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n EDL933
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Potamousis,
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C;Species: Hydra magnipapillata
C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 01-Dec-2000
C;Accession: B41132; S21930
R;Kurz, E.M.; Holstein, T.W.; Petri, B.M.; Engel, J.; David, C.N.
J. Cell Biol. 115, 1159-1169, 1991
                                                                                                                                              RESULT 13
B41132
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C;Superf
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A;Residues: 1-126 <KUR>
A;Cross-references: GB:AE006641; NID:g13815896; PIDN:AAK42717.1; GSPDB:GN00155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, i
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
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A;Residues: 1-115 <STO>
A;Residues: 1-115 <STO>
A;Cross-references: GB:AE004537; GB:AE004091; NID:g9946960; PIDN:AAG04448.1; GSPDB:GN00.
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas A;Reference number: A82950; MUID:20437337
A;Accession: H83514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: H83514
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Miadman, S.; Yuan, Y.; Brody, L.L.; Coulter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein PA1059 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 15-Feb-2002
                                                                                                                        collagen-related protein 2 - Hydra magnipapillata (fragment)
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A; Accession: F90432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession:
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                  Title: Mini-collagens
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 Pens in hydra nematocytes A41132; MUID:92064646
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Coulter, S.N.; Folger, E
                                                                                                                                                                                                                                                                                          Mismatches
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A; Residues: 1-205 <KI
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A; Residues: 1-167 <PAR>
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R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S. e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S. y, P.; Sun, P.M.; Winkler, M.E. J. Bacteriol. 183, 5709-5717, 2001
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S. A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: B97895
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-142 <KUR>
A;Cross-references: EMBL:X61046; NID:g9448; PIDN:CAA43380.1; PID:g9449
A;Note: submitted to the EMBL Data Library, July 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein spr0186 [imported] - Streptococcus pneumoniae (strain C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se A;Reference number: AB0502; PMID:11677608
A;Accession: AH0652
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OM70_YEAST
CWBA_BACSU
RIR1_MYCGE
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DP03_MYCGE
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XAG_XENLA
NP77_XENLA
ATTE_HYACE
MCT1_SHEEP
YFAT_SHEEP
YFAT_EOLI
S1C2_HUMAN
YRB2_YEAST
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"The primary sequence of human pancreatic "The primary sequence of A:75-80(1984).
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"The human collpase gene: isolation, tissue-specific expression.";
Biochemistry 31:7120-7125(1992).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                 use by non-profit institutions as lon modified and this statement is not remove entitles requires a license agreement (S or send an email to license@isb-sib.ch).
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                100.0%;
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                                                                      MW;
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BY SIMILARITY.
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MISSING (IN REF.
Score 7; DB 1; Pred. No. 13; 0; Mismatches
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Pred. No
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PUTATIVE SECRETED (
95E12B06FCB8DCE8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            precursor.
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Mismatches
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8 CRC64;
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Matches 7
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01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Attacin E and F precursor (Immune protein P5).
Hyalophora cecropia (Cecropia moth).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insect Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Benmbycoidea; Saturniidae; Saturniinae; Hyalophora.
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P55869;
                                                                                                                                                                                                                        ATTE_HYACE P01513;
                                                                                                                                                                                                                                                                                                                                                                                                                           Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by ancomplete the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Abberger F., Schueren C., Lepperdinger G., Richter K., Grunz H.; Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-i- SUBCELLULAR LOCATION: Secreted (Probable).
-i- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVEL IN CEMENT GLAND
                                                                                                                                                                                                                                                   HYACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Cement gland;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; (
Amphibia; Batrachia;
SEQUENCE OF 48-235
                                    cecropia
                                                           SEQUENCE FROM N.A.
MEDLINE-91160561; PubMed-2001705;
Sun S.C., Lindstroem I., Lee J.-Y
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
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15-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus laevis (African clawed
                                       "Structure and 
mecropia.";
                                                                                                                                                                                                                                                                                                   142
                                                                                                                                                                                                                                                                                                                          163 DPSLTVR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
SIMILARITY: HIGH, TO XENOPUS XAG.
                                                                                                                                                                                                                                                                                                 DPSLTVR 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                   U82110; AAB49974.1;
                                                                                                                                                                                                                                                                                                                                                  Similarity 7; Conser
                        Biochem. 196:247-254(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel.
(Rel.
(Rel.
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                                               expression
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185
-- 20442 MW;
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36, Last sequence update)
36, Last annotation update)
protein NP77 precursor.
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                                                                                                                                                                                                                                                                                                                                                             3.4%;
                                              Lee J.-Y.,
of the at
                                                                                                                                                                                                                                                                                                                                                 Score 7; DB 1; Pred. No. 13; 0; Mismatches
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PUTATIVE SECRETED PROTEIN

AE3807C926044509 CRC64;
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attacin
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                                              I.;
genes
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                                               Hyalophora
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                                                                                                                                                                                                                                                                                                                                                             Repeat.
SIGNAL
PROPEP
                     Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                             MCT1_SHEEP STANDARD; PRT; 245 AA. P80931; 01-NOV-1997 (Rel. 35, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Mast cell protease 1A precursor (EC 34-21.-) Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
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CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cecropia.";
EMBO J. 3:2065-2070(1984).
-!- FUNCTION: ATTACINS ARE
-!- PTM: ATTACIN F APPEARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boman H.G.;
"Insect immunity. Isolation
corresponding to acidic and
EMBO J. 3:2071-2075(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- MISCELLANEOUS: THERE ARE SIX FORMS OF ATTACIN THAT ARE D INTO TWO GROUPS: ACIDIC (E AND F) AND BASIC (A, B, C, AN -!- SIMILARITY: BELONGS TO THE ATTACIN/SARCOTOXIN II FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Insect immunity. The primary attacin F and its relation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 48-235 FROM N.A.
MEDLINE-86005745; PubMed-3840100;
Boman H.G., Faye I., von Hofsten P., Kockum I
Xanthopoulos K.G., Bennich H., Engstroem A.,
                                                                                                                                        SHEEP
                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "On the primary structures of lysozyme, Hyalophora cecropia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Engstroem
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                                                                                                                                                                                          FLLLVAL
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                                                                                                                                                                                                                                                                                                                                                                                                                            A01775; EWWKEC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      X57715; CAA40886.1; -. X00869; CAA25414.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                   immunity;
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                                                                                                                                                                                                                                                                                                                                                                                                    Antibiotic;
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47
235
231
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169
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TO BE DERIVED BY PROTEOLYTIC DIGESTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and sequence of two cDNA clones basic attacins from Hyalophora cecropia.";
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                                                                                                                                                                                                                                                                                                          ATTACIN E.
ATTACIN F.
GLY-RICH (G1).
GLY-RICH (G2).
                                                                                                                                                                                                                                                        Score 7; |
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                   Hemolymph;
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, Merrifield R.B.,
                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                     Length 235;
                                                             (SMCP-1A).
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                        Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hyalophora
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InterPro; IPR001254; Trypsin.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pemberton A.D., Huntley J.F., Miller H.R.P.;
"Sheep mast cell proteinase-1: characterization
class of dual-specific ruminant chymases.";
Biochem. J. 321:665-670(1997).
-I- FUNCTION: HAS A CHYMOTRYPSIN-LIKE AND TRYPS:
                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 176-185 TISSUE-mast cells; MEDLINE-98343972; PubMed-9677343;
                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS501240; TRYPSIN_DOM;
PROSITE: PS00134; TRYPSIN_HIS;
PROSITE; PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Y14654; CAA74984.1; HSSP; P04187; 2CP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Secretory granules.
-!- TISSUE SPECIFICITY: MUCOSAL MAST CELLS.
-!- SIMILARITY: BELLONGS TO PEPFIDASE FAMILY S1; ALSO KNOWN
TRYPSIN FAMILY. GRANZYME SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97184650; PubMed-9032451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 20-44.
Miller H.R.P., Hur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on substrate specificity."; Biochem. J. 333:801-809(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sheep mast-cell proteinases-1 and structure and molecular modelling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McAleese S.M., Pemberton Miller H.R.P.;
                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Gastric mucosa;
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Mast cell proteases in immunology and biology, pp.203-235,
                                                                                                                                                                                                                                                                                                                                                PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS; S01.142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dekker, New York (1995).
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Mast cell protease 3 precursor (EC 3.4.21.-) (SMCP-3).
Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sheep mast-cell proteinases-1 and -3: cDN structure and molecular modelling of the e on substrate specificity.";
Biochem. J. 33:801-809(1998).
-!- FUNCTION: HAS A CHYMOTRYPSIN-LIKE AND
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PROSITE; PS50240; TRYPSIN_DOM; 1.
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PROSITE; PS00135; TRYPSIN_SER; 1.
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InterPro; IPR001254; Trypsin.
Pfam, PF00089; trypsin; 1.
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                                                                                                                                            TISSUE-Fetal lung;

MEDLINE-99069375; PubMed-9852044;

MEDLINE-99069375; PubMed-9852044;

Sakakibara Y., Yanagisawa K., Katafuchi J., Ringer D.

Sakakibara T., Suiko M., Liu M.-C.;

Nakayama T., Suiko M., Liu M.-C.;

"Molecular cloning, expression, and characterization
SULTIC sulfotransferases that catalyze the sulfonatic
N-hydroxy-2-acetylaminofluorene.";
J. Biol. Chem. 273:33929-33935(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                "Human sulfotransferases SULTIC1 and SULTIC2: gene cloning, and chromosomal localization."; Genomics 65:157-165(2000).
                                                                       MEDLINE-20247255; PubMed-10783263; Freimuth R.R., Raftogianis R.B., Wood T.C., Siciliano M.J., Weinshilboum R.M.;
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T.
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., N
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A.,
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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01-FEB-1995 (
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Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S. V., Whitehead S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                     CHARACTERIZATION.
MEDLINE-98301591;
Taura T., Krebber
                                                                                                                    Taura T., Schlenstedt G., Silver I
"Yrb2p is a nuclear protein that i
homologue.";
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ProDom; PD001218;
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EMBL; AF186263; AAF72810.1;
HSSP; P50224; 1CJM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RANBP2)
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                                                                                                         Biol.
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TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN FETAL LURKIDNEY AND AT LOW LEVELS IN FETAL HEART, ADULT KIDNEY, ON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE SULFOTRANSFERASES FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIDNEY AND AT LOW LEVELS IN FETAL HEART, SPINAL CHORD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIQKLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 7; Conserv
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    Krebber
of the F
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(Rel. 31,
(Rel. 41,
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C H., Silver P.A.; Ran-binding protein
                     PubMed=9636166;
H., Silver P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ascomycota;
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                                                                                                         :31877-31884(1997)
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cota; Saccharomycotina;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
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                                                                                                                                              Prp20p,
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RESULT 11
GCS1_YEAST
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Best Local S
Matches 7
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the Euro
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                                                                                                                                                                                                             Rasmussen S.W.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ
-I- FUNCTION: PLAYS A ROLE IN THE RESUMPTION O
-PROLIFERATION FROM STATIONARY PHASE
-PROLIFERATION FROM STATIONARY PHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTPase activation; SEQUENCE 327 AA;
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                                                                                                                                                                                                                                                                                                                                                                                           Ireland L.S., Johnston G.C., Drebot M
Hoekstra M.F., Singer R.A.;
"A member of a novel family of yeast
the transition from stationary phase
EMBO J. 13:3812-3821(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCS1_YEAST P35197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=94349929; PubMed=8070409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zinc finger protein GCS1 OR YDL226C.
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                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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les 7; Conserv
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SUBUNIT: Interacts with GSP1, XPO1 and PRP20.
SUBCELLULAR LOCATION: Nuclear.
DOMAIN: CONTAINS X-F-X-F-G REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Important for the expert signal (NES) out of the
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              Ween the Swiss Institute of Bloinionmatrics There are no restrictions

Buropean Bioinformatics Institute. There are no restrictions

as its content is in
                                                                                                                                                                     SUBCELLULAR LOCATION: Nuclear (Probable). SIMILARITY: BELONGS TO THE GCS1/GLO3/SPS18 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKKDTKD 66
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S0001325; YRB2.
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(Rel. 28, Last sequence up)
(Rel. 35, Last annotation)
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  this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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he export of protein conaining nuclear
f the nucleus. Stimulates the GTPase
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on update)
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5. 22;
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OF YEAST CELL
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RESULT 12
CPXG_STRSQ
ID CPXG_STRSQ STANDARD;
AC P23296;
DT 01-NOV-1991 (Rel. 20, Cr
DT 01-NOV-1998 (Rel. 20, Lr
DT 15-DEC-1998 (Rel. 37, Lr
DE Cytochrome p450 105C1 (1
GN CYP105C1 OR CHOP.
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                                                                                   Matches
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Zinc-finger;
ZN_FING
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restricted the surpression of the surpression of the swiss of the surpression o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Horii M., Ishizaki T., Paik S.Y., Ma
"An operon containing the genes for
cytochrome p-450-like protein from a
J. Bacteriol. 172:3644-3653(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01412; ArfGap; 1.
PRINTS; PR00405; REVINTRACTNG.
SMART; SM00105; ArfGap; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L24125; AAA50389.1; -. EMBL; Z74274; CAA98805.1; -. SGD; S0002385; GCS1. InterPro; IPR001164; Znf_GCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                            PROSITE; PS00086; CYTOCHROME_P450; 1.
Oxidoreductase; Monooxygenase; Electron transport; Membrane;
BINDING 330 330 HEME (BY SIMILARITY).
                                                                                                                                                                                                                                 Pfam; PF00067; p450; PROSITE; PS00086; CY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                               EMBL; M31939; AAA26718.1; -. HSSP; Q00441; 10XA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-90299781; PubMed-2361941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1931;
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  213 AFLLLVA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 TLSRGWG
                                         39 AFLLLVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLSRGWG
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7; Conserv
                                                                                 Similarity 7; Conser
                                                                                                                                                                                                                                                                           IPR001128; Cyt_P450
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                                                                                                                                                                      381 AA;
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                                                                                   Conservative
                                           45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         utes; Actinobacteria;
Streptomycineae; Str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20, Created)
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                                                                                                                                                                      41703 MW;
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                                                                                                       100.0%;
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Last annotation updat
(EC 1.14.-.-).
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C -> Y (II
FUNCTION)
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                                                                                                                                                                      HEME (BY SIMILARITY); 841B959C9DDEA99C C
                                                                                                                          Score 7;
                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from a Streptomyces
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                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Manome T., Murooka Y., or cholesterol oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IN GCS1-1;
                                                                                                           No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actinobacteridae;
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                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                          There are no rest
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                                                                                                                               Length 381;
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                                                                                                                                                                        CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a collaboration -
MBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          outstation
                                                                                     Gaps
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STANDARD;

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RESULT 14
NOR_FUST
ID NOR, E
AC P2322
DT 01-NK
DT 01-NK
DT 01-K
DT 01-K
DT 01-K
DT 16-Q
C Cyto:
GN CYP5:
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QN NCBI,
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RP SEQUI
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YMK7_YEAST
ID YMK7_YEAST
AC Q03760;
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Matches
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01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
Hypothetical 45.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOR_FUSOX STANDARD; PKI; TO ALL THE PRINCE OF THE PRINCE O
MEDLINE-95096031; PubMed-7798191; Tomura D., Obika K., Fukamizu A., Shoun H.; Notice reductase cytochrome P-450 gene, CYP 55, of the fungus Fusarium oxysporum containing a potential binding-site for FNR, the transcription factor involved in the regulation of anaerobic growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wypotnetical 45.2 kDa protein in ZDS2-URA5 in YML107C OR YM8339.12.
                                                                                                                                                                                                                                                                                              "Nucleotide sequence of the unique nitrate/nitrite-inducible cytochrome P-450 cDNA from Fusarium oxysporum.";
J. Biol. Chem. 266:10632-10637(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomy Hypocreales; mitosporic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reductase) (P450 NOR).
CYP55A1 OR CYP55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-S288C / AB972;
Skelton J., Churcher C.M., I
Submitted (MAY-1995) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND STRAIN-MT-811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusarium oxysporum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetales;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes.
                                                                                                                                                                                                  SEQUENCE FROM
STRAIN=MT-811;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Kizawa H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91244845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical SEQUENCE 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5507;
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                                                                                                                                                                                                                                                                                                                                                                                                             Shoun H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               386 AA;
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                                                                                                                                                                                                                                N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=2037602;
D., Oda M., Fuk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ascomycota; Pezizomycotina; sporic Hypocreales; Fusarium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35,35
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE
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e EMBL/GenBank/DDBJ databases.
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Lee D.-S., Park S.-Y., Yamane K., Obayashi E., Hori H.
"Structural characterization of n-butyl-isocyanide compounded by the cytochromes P450nor and P450cam.";
Biochemistry 40:2669-2677(2001).
1- FUNCTION: INVOLVED IN A DISSIMILATORY REDUCTION OF AS A NUTRATE NATURE.
1- INDUCTION: BY NITRATE_NITRITE.
1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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J. Biol. Chem. 275:4816-4826(2000).
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Nakahara K., Shoun H., Obayashi E., Nakamura H., Iizuka T., S
"Crystal structure of nitric oxide reductase from denitrifylm
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J. Biochem. 116:88-94(1994).
                                                                                                  SEQUENCE
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AFLLLVA 238
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402 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-IFO 30561;
MEDLINE-97163854; PubMed-9010609;
Kudo T., Tomura D., Liu D.L., Dai X.Q., Shoun H.;
Kudo T., Tomura D., Liu D.L., Dai X.Q., Shoun H.;
"Two isozymes of P450nor of Cylindrocarpon tonkinense: molecular cloning of the cDNAs and genes, expressions in the yeast, and the putative NAO(P)H-binding site.";
Biochimie 78:792-799(1996).
-1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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15-DEC-1998 (Rel. 37, Created)
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Cytochrome P450 55A2 (EC 1.14...) (Cytochrome P450NOR1).
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Pfam; PF00067; p450; 1.
PRINTS; PR00359; BP450.
PROSITE; PS00086; CYTOCHROME_P450; FALSE_NEG.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Neonectria.
NCBI_TaxID=42744;
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Q96hp9 homo sapien	4	4 30	3.4	7	43
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Q9plm7 chlamydia	16	30	3.4	7	41
Q9wrt4 macaca mula	12	4 29	3.4	7	40
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Q51756 pseudomonas	2	4 29	3.4	7	38
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Q9skil arabidopsis	10	4 27	3.4	7	5
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Q9j218 macaca mula	12	4 25	3.4	7	30
8	10	4 25	3.4	7	29
Q9ewr7 streptomyce		4 22	3.4	7	28
Q95xx7 caenorhabdi		4 18	3.4	7	27
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ALIGNMENTS

095994 RESULT 1 Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF038451; AAC82614.1; -.
EMBL; AF007791; AAC77358.1; -.
EMBL; AF008867; AAF22484.1; -.
EMBL; BC015503; AAH15503.1; -.
EMBL; BC015503; AAH15503.1; -.
EMBL; BC015503; AAH15503.1; -.
EMBL; BC015503; BAH15503.1; -.
EMBL; BC015503; BAH15503.1; -. XAG-2, 1 lines."; 095994;
01-MAY-1999 (TREMBLREL 10, Created)
01-MAY-1999 (TREMBLREL 10, Last sequence update)
01-DEC-2001 (TREMBLREL 19, Last annotation update)
SECRETED CEMENT GLAND PROTEIN XAG-2 HOMOLOG (ANTERIOR GRADIENT (XENEPUS LAEVIS) HOMOLOG). Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Zhang J.S., Smith D.I.; "Human homolog of XAG is differentially expressed in tumors."; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases. Thompson D.A., Weigel R.J.; "hAG-2, the human homologue of the Xenopus laevis cement gland gen XAG-2, is coexpressed with estrogen receptor in breast cancer cell 095994 SEQUENCE SEQUENCE FROM N.A.
TISSUE-COLON ADENOCARCINOMA; Biochem. Biophys. Res. Commun. 251:111-116(1998). SEQUENCE FROM N.A. MEDLINE=99009231; PubMed=9790916; TISSUE-BREAST SEQUENCE FROM N.A. NCBI_TaxID=9606; HAG-2/R OR HAG-2/C PRELIMINARY; ¥. F271B1BD377BEE11 CRC64; 175 ₽

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                                                                                                                                C STRAIN-C57BL/6J; TISSUE-PANCREAS;

X MEDLINE-21085660; PubMed-1121781;

X MEMBLY J., Shinagawa A., Shibata Y., Konno H., Adachi J., Fukuda S., Xamanaka I., Xalxawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Xalxawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Xakota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T., Xakota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T., Xakota K., Matsuda T., Nishido I., King B., Kochiwa H., Xahido I., Pesole G., Quackenbush J., Xakota M., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Xakota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Xakota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Xakota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Xakota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Xakota K., Okido T., Furuno M., Aono H., Baldarelli M., Gariboldi M., Xakota K., Ting B., Kingwald M., Rodriguez I., Sakamoto N., Jangwald M., Rodriguez I., Sakamoto N.,
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"hAG-2, L.
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01-NOV-1998
01-DEC-2001
                                                             Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L. Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Ródentia;
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                                 Nature 409:685-690(2001).
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Submitted (AUG-2001) to the EN
EMBL; AB016592; BAA32044.1; -
EMBL; AF044262; AAC72705.1; -
EMBL; AK007677; BAB25181.1; -
EMBL; BC013334; AAH13334.1; -
                                                                                                        MLR6569 PROTEIN.
MLR6569.
Rhizobium loti (Mesorhizobium loti).
Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision;
Bacteria; Protecae; Mesorhizobium.
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Q90Y05;
01-DEC-2001
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01-0CT-2001
01-0CT-2001
STRAIN-MAFF303099;
MEDLINE-21082930; PubMed-11214968;
Maneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasam
Matanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura
Mishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic
                                                                                                                                                                                                                                                                                                                                                                                    "Three novel genes expressed in the anterior | laevis embryo."; laevis embryo."; to the EMBL/GenBank/DDBJ Submitted (OCT-2000) to the EMBL/BenBank/DDBJ EMBL; AF314056; AAL26844.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CEMENT GLAND-SPECIFIC PROTEIN CGS.
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
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                                                                                            SEQUENCE FROM N.A.
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Pred. No.
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    symbiotic bacterium
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Q62943;
  WEDLINE=20036896; PubMed=10567266; White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson White O., Elsen J.A., Heidelberg J.F., Nelson W.C., Richardson Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski
                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2001 (TrEMBLrel. 18, Last annotation updat
ACYL-COA DEHYDROGENASE, PUTATIVE.
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MEDLINE-97080538; PubMed-8921883;
Thomas M.B., Haines S.L., Akeson
"Chemoreceptors expressed in tast
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SEQUENCE
                                                                                                                                                                Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus
NCBI_TaxID=1299;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-NOV-1996 (TIEMBLIEL. 01, Last sequence update)
01-DEC-2001 (TIEMBLIEL. 19, Last annotation update)
TASTE BUD RECEPTOR PROTEIN TB 567.
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DNA Res. 7:331-338(2000).
EMBL; AP003009; BAB52836.1;
                                                                                                                              SEQUENCE
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EMBL; U50948; AAC5
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                                                                                                                                                                                                                                                                                                                                     Q9RYQ8;
                                                                                                                                                                                                                                                                                                                                                            Q9RYQ8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissues
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[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 GDQLIWTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLLVALSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00001; Thm.1; 1.

PF00001; Ttm.1; 1.

PE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

PE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
8; Conserv
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200 AA;
                                                                                                                              FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             315 AA;
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ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.9%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                            N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35556 MW;
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in taste, ol
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Pred. No
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Sciurognathi;
                                                                                                                                                                                        group;
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. 8.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 315;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
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M., Shen M.,
Zalewski C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                        Deinococcus
                                                              Peterson J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murinae;
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RESULT
Q9VB20
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Q960R8
Qy
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Best Local S
Matches 8
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Best Local S
Matches 8
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Q9VB20;
01-MAY-2000
01-MAY-2000
01-DEC-2001
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01-DEC-2001
01-DEC-2001
LD38671P.
     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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Ketchum K.A., N
Fraser C.M.;
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-Y, CN BW SP;
STRAIN-Y, CN BW SP;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlsor Champe M., Chavez C., Dorsett V., Farfan D., Frise E., Ge Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Munga Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY051898; AAK93322.1;
EMBL; AY051898; AAK93322.1;
SEQUENCE 1232 AA; 136912 MW; CEF6003D6939A6DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q960R8
Q960R8
                                                             CG5634 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                        Ephydroidea; Drc
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata;
Pterygota; Neoptera; Endopterygota; Diptera
Ephydroidea; Drosophilidae; Drosophila.
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Pfam; PF00441; Acyl-CoA_dh; 2.
Pfam; PF02770; Acyl-CoA_dh_M; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      radiodurans R1.";
Science 286:1571-1577(1999).
Science 286:1571-1577(1999).
EMBL; AE001863; AAF12388.1;
TIGR; DRA0250; -
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ilarity 100.0%;
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Conservative
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Nelson K.E.,
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13,
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Salzberg S.,
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Pred. No. 26;
0; Mismatches
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                                                                                  sequence update) annotation updat
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                                        Hexapoda;
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a; Brachycera;
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                              Brachycera;
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                                        Insecta;
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ingall C.J.
ig S., Wan
                              Muscomorpha;
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler R., Charler R., Danke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleisohmann W.,
RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Correll J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Correll J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Liu X., Mattei B., McIntosh T.C., McIed J., Ketchum K.A.,
RA Liu X., Mattei B., McIntosh T.C., McIedd M.P., McPherson D.,
RA McMalov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Yeln S.M., McOdage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yeln S.M., McModage T., Worley K.C., Wu D., Yang S., Zhou Y.,
RA Yeln S.M., McModage T., Worley K.C., Wu D., Zhong S., Zhong Y.,
RA Schorz S., Laperson S., Scholer S., Zhu X., Smith H.O.,
RA Yeln S.M., McModage T., Worley K.C., Wu D., Zhong S., Zhong Y.,
RA Schorz S., Short M., Zhong S., Zhong W., Zhong S., Zhong Y.,
Short M., Short M.,
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                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                    Matches
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InterPro; IPR001798; Kelch.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR002165; Plexin_repeat
InterPro; IPR0031659; PSI.
InterPro; IPR003659; PSI.
InterPro; INT
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EGF-11ke
SEQUENCE
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EMBL; AE003761; AAF56723.1; --
HSSP; P02468; 1KLO.
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475
                                                                          179
RLYAYEPA 482
                                                                              RLYAYEPA 186
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; PS01180; CUB; 2.
; PS00022; EGF_1; 2.
; PS01186; EGF_2; 1.
                                                                                                                                                        Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                           domain;
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AA; 142507 M
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EGF-like.
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01-DEC-2001
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Kang W., Tristem M., Maeda S., Crook N.E., O'Reilly D.R.;
"Identification and characterization of the Cydia pomonel
granulovirus cathepsin and chitinase genes.";
J. Gen. Virol. 79:2283-2292(1998).
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Viruses; dsDNA viruses,
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         NADH
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MEDLINE-97380577; PubMed-9237352;
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Theilmann D.A., Chantler J.K., Stweart S., Flipsen H.T., Vlak J.M.,
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יטא-1998 (TremBLrel. 06, Last sequence update)
יפל-2001 (TremBLrel. 19, Last annotation update)
DEHYDROGENASE SUBUNIT 6 (FRACMPNT)
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01-JAN-1999 (TrEMBLrel. 09, Last sequence of the control of
                                                                                                               Submitted (DEC-1998) to the EMBI EMBL; U28382; AAC98518.1; -. InterPro; IPR001064; Crystallin. PROSITE; PS00225; CRYSTALLIN_BBT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yang K., Han L., Ayer S.W., Vining L.C. "Accumulation of the angucycline antibi disruption of an oxygenase gene in the cluster of Streptomyces venezuelae."; Microbiology 142:0-0(0).
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Q56157;
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Submitted (JUN-1995)
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MEDLINE=96146057; PubMed=8581159;
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Mitochondrial DNA variation and
northern redbelly dace (Phoxinus
Mol. Ecol. 4:745-753(1995).
EMBL; U34407; AAC01504.1;
InterPro; IPR001457; Oxidored_q3.
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Matches 7; Conserv
                                                        InterPro; IPR000504; RRM.
Pfam; PF00076; rrm; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
SEQUENCE 109 AA; 12349 M
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01-MAR-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9GZT3;
                                                                                                                                                        SEQUENCE FROM N.A.

Xu X., Yang Y., Gao G., Xiao

Submitted (MAY-2000) to the E

EMBL; AF271779; AAG44790.1; -

EMBL; AF253980; AAG44629.1; -
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                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   crenarchaeon, Aeropyrum pernix Kl."; DNA Res. 6:83-101(1999).
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01-MAR-2001
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-··heria; Primates; (
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EMBL/GenBank/DDBJ
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Score 7; I
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                                                          8BDCB6EA244F17B8 CRC64;
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RESULT Q97SVT.
ID Q97SVT.
ID Q9 AC Q9 AC Q9 AC Q9 OC OC ST.
OC ST.
RRN SEN NC ST.
RRA TEER RA UMR RA UMR RA HOOR RA HO
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Q9KXA4
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Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
Peterson S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.,
"Complete genome sequence of a virulent isolate of Streptococcus
pneumoniae.";
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01-0CT-2001 (TremBLrel. 18,
01-0CT-2001 (TremBLrel. 18,
01-DEC-2001 (TremBLrel. 19,
CONSERVED DOMAIN PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                       O9KXA4;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 12.4 KDA PROTEIN.
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Science 293:498-506(2001).
EMBL; AE007335; AAK74387.1; -.
TIGR; SP0207; -.
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"Complete nucleotide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the enterohemorrhagic Escherichia coli 0157:H7 derived from the Sakai outbreak.";
                                                                        MEDLINE-20198780; PubMed-10734605; Yutsudo C.H., Makino K., Yokoyama K., Kubota Y., Yutsudo C.H., Kurokawa K., Ishii K., Hattori M., Tatsuno I., At Yamamoto K., Ohnishi M., Hayashi T., Yasunaga T., Sasakawa C., Shinagawa H.;
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                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Escherichia.
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                                                                                                                                                                                                                                                                                                                                              gamma subdivision; Enterobacteriaceae;
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b; Pred. No. 37;
0; Mismatches
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Best Local
                                                                                               Hypothetical SEQUENCE 11
                                                                                                               Genes Genet. Syst. 74:227-239(1999).
EMBL; AP000422; BAA94180.1; -.
                                   197 KALKILK 203
                          108 KALKLLK 114
                                                           l Similarity
7; Conserv
                                                                                               11 protein.
114 AA; 1
                                                             Conservative
                                                                                                12409 MW;
                                                                     3.4%;
9,
2002, 16:44:07
                                                              0;
                                                                     Score 7;
Pred. No.
                                                                                                ABF77340011439AB CRC64;
                                                              Mismatches
                                                                      DB 2;
o. 37;
                                                              0,:
                                                                              Length 114;
                                                              Indels
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Search completed: October Job time : 30 secs

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Run
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Word size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                       NO.
    score greater than and is derived by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length: 0
length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OLIGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            October 9, 2002, 16:42:22; Search time 18 Seconds (without alignments) 279.537 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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   24425594 residues
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US-08-916-576B-2
US-09-247-155-174
US-09-247-155-174
US-09-247-155-174
US-08-916-576B-8
US-08-916-576B-8
US-08-916-576B-7
US-08-916-576B-7
US-08-93-359-28
US-08-471-496-9
US-08-471-496-9
US-08-471-496-2
US-08-471-496-2
US-08-63-552-1
PCT-US93-05704-13
US-08-063-552-2
PCT-US93-05704-2
US-08-063-552-2
PCT-US93-05704-2
US-08-063-552-2
PCT-US93-05704-2
US-08-063-552-2
PCT-US93-05704-3
US-08-944-133-13
US-08-944-133-13
US-08-944-133-13
US-08-194-981E-39
US-08-194-981E-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    parameters:
            Sequence 6, Appli
Sequence 7, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 28, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 14, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
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Sequence 106, App
Sequence 174, App
Sequence 6, Appli
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US-08-545-809A-123	US-08-545-809A-116	US-08-545-809A-114	US-08-545-809A-140	US-08-545-809A-118	US-08-545-809A-92	US-08-858-207A-273	US-09-309-487-22	US-09-309-487-21	US-09-309-487-29	US-09-309-487-16	US-09-309-487-14	US-09-326-039-2	US-09-227-357-216	US-08-714-524D-31	US-08-484-101B-31	US-08-530-010-31	US-08-194-981E-44
Sequence 123, App	Sequence 116, App	Sequence 114, App	•	Sequence 118, App		٣.	•	Sequence 21, Appl	•	Sequence 16, Appl	•	Sequence 2, Appli	Sequence 216, App	`	Sequence 31, Appl	•	Sequence 44, Appl

ALIGNMENTS

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RESULT 1
US-08-916-576B-2
                                                                       ; MOLECULE TYPE: protein US-08-916-576B-2
                                                                                                                                                   NAME: STEFFE, EXIC K.

REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
I ENGRIP. 175 5615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08916576B Patent No. 6171816
Query Match
Best Local Similarity
Matches 175; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
PRIOR APPLICATION UNDER: US 60/024,347
PILLING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
ANTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,576B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                               TYPE: amino acid
TYPE: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: STERNE
STREET: 1100 NEW
CITY: WASHINGTON
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RY: US
20005-3934
                                                                                                                                        175 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YU, GUO-LIANG
DILLON, PATRICK J.
EBNER, REINHARD
 Conservative
                85.0%;
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0;
             Score 175; DB 4; L. Pred. No. 1.3e-159;
 Mismatches
                                 Length 175;
Indels
 0;
Gaps
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32 MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE 91

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; LOCATION: -20..-1
US-09-247-155-106
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CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER APPLICATION NUMBER: 60/099,273
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                                                                                                                                                                                      Sequence 174, Application US/09247155A Patent No. 6312922
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Best Local Similarity 100.0%; Pred. No. 1.3e-159;
Matches 175; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
SOFTWARE: Patent.pm
SEQ ID NO 106
LENGTH: 175
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Patent No. 63129
                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                APPLICANT: Dumas wilne Edwards, Jean-Baptiste APPLICANT: Duclert, Aymeric APPLICANT: Bougueleret, Lydie TITLE OF INVENTION: Complementary DNAS FILE REFERENCE: GENSET.021A CURRENT APPLICATION NUMBER: US/09/247,155A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: GENSET.021A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Complementary DNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dumas Milne Edwards, Jean-Baptiste APPLICANT: Duclert, Aymeric
EARLIER APPLICATION NUMBER: 60/074,121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bougueleret, Lydie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                92 ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                     61 ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP 120
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EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
NUMBER OF SED ID NOS: 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Sin
Matches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patent.pm
SEQ ID NO 174
LENGTH: 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08916576B Patent No. 6171816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE: SIGNAL NAME/KEY: SIGNAL LOCATION: -20..-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                          TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: UNSURE LOCATION: 40,41,43,60,70,76,82,86,105,107
OTHER INFORMATION: Xaa = any one of the twenty amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,576B
                                 SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
                                                                                                                                                                       FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,0
                                                                                                                                                                                                                                       CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
FILING DATE: 23-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                 REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 110 CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYE
                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: STERNE, KESSLER, GO 1100 NEW YORK AVENUE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YU, GUO-LIANG
DILLON, PATRICK J.
EBNER, REINHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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100.0%; Pr
                                                                                                                                                                             36,688
                                                                                                                                                                                                                                                           60/024,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 59;
Pred. No.
                                                                                                                                                            1488.0500001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GOLDSTEIN & FOX, P.L.L.C
E, SUITE 600
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APPLICANT:

DILLON, PATRICK J.

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RESULT 6
US-08-916-576B-7
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US-08-916-576B-8
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             Sequence 7, Application US/08916576B Patent No. 6171816 GENERAL INFORMATION:
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                                                                                                                                                                                               Query Match
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APPLICANT:
APPLICANT:
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REFERENCE/DOCKET NUMBER: 14/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 APPLICANT:
                                                                                                                                                                                                                                       TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
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TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBER OF SEQUENCES:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                             170 amino acids
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YU, GUO-LIANG
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100.0%;
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Pred. No.
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RESULT 7
US-08-063-552-10
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                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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PRIOR APPLICATION NUMBER: US 6(
APPLICATION NUMBER: US 6(
FILING DATE: 23-AUG-1996
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                      APPLICANT: Edwards, TITLE OF INVENTION:
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ATTORNEY/AGENT INFORMATION:
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NUMBER OF SEQUENCES:
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CITY: Pasadena
STATE: California
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nes 7; Conserv
CLASSIFICATION:
             APPLICATION NUMBER: UFILING DATE: 19930514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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100.0%;
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                                                                                                                                                                                                                                                                      Vesicle Membrane Transport Proteins
                                                                                                                                                                                                                                                                                   Robert H
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Pred. No
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Query Match
Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: Edwards, Robert H
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                                                                                   TOPOLOGY: line
MOLECULE TYPE: P
HYPOTHETICAL: NC
FRAGMENT TYPE: 1
ORIGINAL SOURCE:
ORGANISM: Ratt
                                                                                                                                                                                                                             TELEFAX: (818) 795-6321 INFORMATION FOR SEQ ID NO: 10:
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                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION MADE: PC-04/1503-065704
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LENGTH: 220 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 220 amino acid
                                                                                                                                                                                                                                                            TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9067-1PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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CITY: Pasadena
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DGY: linear
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           3.4%; Score 7; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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100.0%; Pr
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s; Pred. No. 40;
0; Mismatches
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            Mismatches
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                         DB 5;
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           0
                                        Length 220;
           Indels
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           Gaps
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GENERAL INFORMATION:
APPLICANT: Bach, Lisbeth
APPLICANT: Obmann, Anders
APPLICANT: Breinholt, Jens
APPLICANT: Fuglsang, Claus C.
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US-08-773-870-1
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                                                                                                                         RESULT 10
US-08-993-359-28
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                                                                                           Sequence 28, Application US/08993359A Patent No. 6039942
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                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
LIBRARY: Consensus
CLONE: Consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K
                                                                                                                                                                                                  164 PSLTVRA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                   132 PSLTVRA 138
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                                                                                                                                                                                                                                      3.4%; Score 7; Local Similarity 100.0%; Pred. Notes 7; Conservative
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3174 POI
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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APPLICANT:

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Best Local Similarity
"htches 7; Conserva
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US-08-471-496-9
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; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-08-993-359-28
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                                                                                                                                                                          APPLICATION NUMBER: US/08/471,496
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US95/02645
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
NAME: STEFFE, ERIC K
16 688
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EARLIER FILING DATE: 1997-12-01
EARLIER APPLICATION NUMBER: 60/046,082
EARLIER APPLICATION NUMBER: 60/046,082
EARLIER FILING DATE: 1997-05-09
NUMBER OF FEET TO THE PROPERTY OF THE PROPER
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CURRENT FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 1480/96
EARLIER FILING DATE: 1996-12-20
EARLIER APPLICATION NUMBER: 1481/96
EARLIER FILING DATE: 1996-12-20
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EARLIER FILING DATE: 1997-03-18
EARLIER APPLICATION NUMBER: 0529/97
EARLIER FILING DATE: 1997-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH: 442
                               REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 144
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: ROSEN, CRAIG
TITLE OF INVENTION: HUMAN AMINE TRANSPORTER
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383 RLSCAGT 389
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100.0%; Pred. No.
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US-08-894-840-9
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US-08-894-840-9
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RESULT 13
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                                                                                                      Query Match
Best Local Similarity
Matches 7; Conserv
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Best Local Similarity 100
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: LI, YI
                                                                                                                                                                                                                                                 TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 465 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/00
FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CAO, LIANG
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: HUMAN AMINE TRANSPORTER
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                           189 ALLLDNM 195
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                                                                                                                                                                                                    STRANDEDNESS: not TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                            30 ALLLDNM
                                                                                                                                                                                                                                   TYPE: amino acid
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                                                                                                      3.4%; Score 7; DB; ilarity 100.0%; Pred. No. 77 Conservative 0; Mismatches
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100.0%; Pred. No.
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E, SUITE 600
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5. 77;
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US-09-139-675-9
; Sequence 9, Application US/09139675A
; Sequence 6117426
; Patent NO. 6117426
; GENERAL INFORMATION:

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LENGTH: 470 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-496-2
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Best Local Similarity
Watches 7; Conserva
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APPLICANT: Rosen, Craig
APPLICANT: Rosen, Craig
TITLE OF INVENTION: Human Amine Transporter
FILE REFERENCE: 1408.0830003
CURRENT APPLICATION NUMBER: US/09/139,675A
CURRENT FILING DATE: 1998-08-25
EARLIER APPLICATION NUMBER: WO PCT/US95/02645
EARLIER APPLICATION NUMBER: WO PCT/US95/02645
EARLIER APPLICATION NUMBER: US 08/471,496
EARLIER FILING DATE: 1995-06-06
RUMBER OF SEQ ID NOS: 9
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US-08-471-496-2
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SEQ ID NO 9
LENGTH: 465
TYPE: PRT
                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,496
FILING DATE: 06-JUN-1995
CLASSIFICATION OBTA:
APPLICATION NUMBER: WO PCT/US95/02645
APPLICATION NUMBER: WO PCT/US95/02645
APPLICATION NUMBER: 36,688
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0830001
TELECOMMUNICATION INFORMATION:
TELECHONE: (202) 371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIA
APPLICANT: ROSEN, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Applic Patent No. 5798223
Query Match
Best Local Similarity
                                                                                                                                                                       TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: CAO, LIANG
APPLICANT: ROSEN, CRAIG
TITLE OF INVENTION: HUMAN AMINE TRANSPORTER
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 470 amino acid
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3.4%;
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 Mismatches

  Score 7;
Pred. No.
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                    Length 470;
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                                                                                                                 Query Match
Best Local Similarity
Thes 7; Conserve
                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-894-840-2
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Search completed: October 9, Job time: 19 secs
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                                                                                                                                                                                                                                                         TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 470 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: COSEN, CRAIG A.
TITLE OF INVENTION: HUMAN AMINE TRANSPORTER
NUMBER OF SEQUENCES: 9
CORRESPONDENT. ..
                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,6
                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/894,840 FILING DATE: 29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                  189 ALLLDNM 195
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                                                                  30 ALLLDNM 36
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ZIP: 20005-3934
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                                                                                                                                                                                                                                                TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C STREET: 1100 NEW YORK AVENUE, SUITE 600
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100.0%; Pred. No. 78;
ive 0; Mismatches
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                    2002, 16:45:11
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gb_pat:AX192616
gb_pat:AX341186
gb_pat:AX341116
gb_pat:AX36839
                       gb_pat:AX231718
gb_pat:AX193063
gb_pat:AR123830
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gb_pat:AX341139
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gb_pat:AR123828
gb_pat:AX067336
gb_pat:AX341388
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Sequence
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gb_ro:BC013334
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gb_ro:AB016592
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gb_pr:AF007791
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gb_pat:AR177410
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gb_pat:AX341084
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Query length:
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Database length: 1873333701
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gb_pat:AX341229
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-Q-/cgqn2_1/USPTO_spool/US99674266/runat_08102002_093324_26161/app_query.fasta_1.271
-Q-/cgqn2_1/USPTO_spool/US99674266/runat_08102002_093324_26161/app_query.fasta_1.271
-DB-GenEmb1 -QFMF-fastap -SUFFIX-p2n.rge -GAPOP-12.000
-GAPEXT-4.000 -MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000
-QGAPEXT-0.005 -XGAPOP-10.000 -YGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-9.500
-DELOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-9.500
-DELOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-9.500
-DELOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPOXT-9FG
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-PCT
-THR_MAX-100 -THR_MIN-0 -ALIGN-15 -DOXALIGN-200 -OUTFMT-PfS
-NORM-0xt -HEAPSIZE-500 -MINICH-15 -MAXIEN-200000000
-USER-US09674266_@CGN1_1_3973 -NCPU-6 -ICPU-3 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -NO_XLPXY -WAIT -THREADS-1
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US-09-674-266A-181
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version
                                                                         BC015503 Homo sapiens, anterior AR123828 Sequence 1 from patent AX067336 Sequence 1635 from patent AX067336 Sequence 61 from patent AX067336 Sequence 1635 from patent AX341388 Sequence 1635 from patent AX341234 Sequence 1481 from patent AX341234 Sequence 149 from patent AX341231 Sequence 71 from patent AX351468 Sequence 215 from patent AX351468 Sequence 78 from patent AX14213 Sequence 78 from patent AX144213 Sequence 78 from patent AX144213 Sequence 18 from patent AX144213 Sequence 18 from patent AX144213 Sequence 18 from patent AX1423158 Sequence 18 from patent AX192616 Sequence 183 from patent AX341186 Sequence 133 from patent AX341186 Sequence 32 from patent AX341186 Sequence 32 from patent AX340568 Sequence 2131 from patent AX340568 Sequence 2131 from patent AX341139 Sequence 1771 from patent AX341139 Sequence 51 from patent AX341139 Sequence 51 from patent AX341139 Sequence 7 from patent AX341139 Sequence 7 from patent AX31139 Sequence 106 from patent AX31139 Sequence 107 from patent AX31139 Sequence 108 from patent AX31130 Sequence 108 from patent AX31131 Sequence 1
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Documentation

I AX011612 Sequence 8 from Pater

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I AF088867 Homo sapiens putative
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KEYWORDS
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117 aLeuLysLysValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluG
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gb_pat:AX302898
gb_pat:AX322727
gb_pat:AX192553
gb_pat:AR123858
gb_pat:AX341299
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US-09-674-266A-181 x AX011612
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LOCUS AX011612
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              LysProLeuMetIleIleHisHisLeuAspGluCysProHisSerGlnAl 117
                                                                                                                                                                                 AlaArgAspThrThrValLysProGlyAlaLysLysAspThrLysAspSe
                                                                            leTrpThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn
AAACCCTTGATGATTATTCATCACTTGGATGAGTGCCCACACAGTCAAGC
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                                                                                                                        TCGACCCAAACTGCCCCAGACCCTCTCCAGAGGTTGGGGTGACCAACTCA
                                                                                                                                       rArgProLysLeuProGlnThrLeuSerArgGlyTrpGlyAspGlnLeuI
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Sequence 8 from Patent W09955858.
AX011612
AX011612.1 GI:9998136
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SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINDMANN BERND (DE); ROSENTBAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN (DE); FILARSKY CHRISTIAN (DE)
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7 Sequence 2 from Pat
3 Sequence 120 from P
8 Sequence 36 from pa
9 Sequence 1546 from
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seq_documentation_block:
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US-09-674-266A-181 x AX015056
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Quality: 1063.00
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                                                                                             AGACTCAGCTGTGCTGGCACACTCAGCGGCTCTGGACCGCATCCTAGCCG
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                                                                                                                                                                                                                                                                                                                                                             Patent: WO 9953040-A 265 21-OCT-1999;
SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
                                                                                                                                                                                                                                                                                                                                                                                     Human nucleic acid sequences from ovarian tumour tissue Patent: WO 9953040-A 265 21-OCT-1999;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Zhang, J.S. and Smit
Direct Submission
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Zhang, J.S. and Smith,
Human homolog of XAG
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens putative secreted AF088867
                                                                                                                                                            Submitted (30-AUG-1998) Pathology and Lab. 200 SW 1st St., Rochester, MN 55905, USA
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AF088867
                                                                                                                                                                                                                               Unpublished
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translation="MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTL/
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Primates;
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QFVLLNLVYETTDKHLSPDGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALL
,LDNMKKALKLLKTEL"
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PRI 03-DEC-1998
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TITLE
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alignment_scores:
Quality: 1002.00
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US-09-674-266A-181 x AF038451
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                                             102 TCTCCTACACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAAAAG
                                                                                                                                                                                                                 52 AGTTGCCATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCC
                                                                                                                                                    gValAlaMetGluLysIleProValSerAlaPheLeuLeuLeuValAlaL
                                                                  euSerTyrThrLeuAlaArgAspThrThrValLysProGlyAlaLysLys
AspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA, complete AF038451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (09-DEC-1997) Surgery, Road, MSLS Building, Room P228,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1077)
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/db_xref==0ci=3779226"
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OFVLLNLVYETTDKHLSPDGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALL
LDNMKKALKLLKTEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to Homo sapiens protein hAG-2/C deposited under GenBank Accession Number AF007791, and to Xenopus laevis cement gland-specific proteins np77 and XAG-2 deposited under GenBank Accession Numbers U82110 and AF025474, respectively"
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59. .586
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/db_xref="taxon:9606"
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/note="isolated from estrogen
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                                                                                                                                                                                                                       Direct Submission
Submitted (21-DEC-1998) Laboratory of Medicine and Pathology, Clinic, 200 SW 1st Street, Rochester, MN 55905, USA
                                                                                                                                                                                                                                                                 Unpublished
2 (bases 1 to 1701)
2 hang, J.S. and Smith, D.I.
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Zhang, J.S. and Smith, D.I.
Identification of human h
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
         /gene="HPC8"
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OFVLLNVYETTOKHLSPDGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALL
                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                  /gene="HPC8"
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LOCUS BC015503
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                                                                                                                                  seq_name:
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                                                                                homolog,
                                                                                             PRI 29-OCT-2001
                                                                                clone
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JOURNAL REFERENCE AUTHORS TITLE

FEATURES

source

gene

/cell

JOURNAL

REFERENCE AUTHORS TITLE

SOURCE ORGANISM

HOMO

sapiens

VERSION ACCESSION DEFINITION

AF115926.1

KEYWORDS

seq_documentation_block: seq_name: gb_pr:AF115926

502 179 452 163 402

552 196 146

352

129

302 113 252

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REMARK
COMMENT
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                                                                      erTyrThrLeuAlaArgAspThrThrValLysProGlyAlaLysLysAsp
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 665281: Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, Web site:

http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (01-CCT-2001) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
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Tissue Procurement: ATCC
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Sequence 40 from Patent W00078960.
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                                                                                                                                                                           Yugiu, J. and Mitcham, J.L. Compositions and methods
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Mammalia; Eutheria;
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10-JAN-2002

and Bougueleret, L.

96.923

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seq_documentation_block:
LOCUS
AR177367
DEFINITION Sequence 61 fi
ACCESSION AR177367
VERSION AR177367.1 G1
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ORIGIN
                                                      seq_name: gb_pat:AR177367
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                                                                           TGCTGAAGACTGAATTG
                                                                                                                 ACCTGCAGATACAGCTCTGTTGCTTGACAACATGAAGAAAGCTCTCAAGT
       1689 bp
Sequence 61 from patent US 6312922.
ARI/77367
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AR177367.1 GI:17919722
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1. .593
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/db_xref="taxon:9606"
145 c 120 g 13
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                            PAT
                            17-DEC-2001
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AUTHORS
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FEATURES
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SOURCE
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Quality:
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ORIGIN
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                   etLysLysAlaLeuLysLeuLeuLysThrGluLeu
                                                                                  CysProHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIl 128
                                                                                                                                                                                                                                                                                         yTrpGlyAspGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrL
                                                                                                                                                                                                                                                                                                                                                                    laLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAlaLys
                                                       ysSerLysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGlu
                                                                                                                                                                                                                                                                              TTGGGGTGACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATA
          TGAAGAAAGCTCTCAAGTTGCTGAAGACTGAATTG
                                              TCGTCTCTATGCTTACGAACCTGCAGATACAGCTCTGTTGCTTGACAACA
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Edwards, J.-B. Dumas. Milne.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unknown
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REFERENCE
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SOURCE
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LOCUS AX341084
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US-09-674-266A-181 x AX341084
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AspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnAr 179
                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent: WO 0196388-A 1331 20-DEC-2001; CORIXA CORPORATION (US)
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/db_xref="taxon:9606"
143 c 113 g 13
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SOURCE
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US-09-674-266A-181 x AX341234
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ORIGIN
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Percent Similarity:
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AX341234
                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent: WO 0196388-A 1481 20-DEC-2001;
CORIXA CORPORATION (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jiang,Y., Harlocker,S.L. and Secrist,H. Compositions and methods for the therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Aammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/db_xref="taxon:9606"
153 c 116 g 14
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BASE COUNT
ORIGIN
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KEYWORDS
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US-09-674-266A-181 x AR177410
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LOCUS AR177410
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Percent Similarity:
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AR177410
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Edwards, J.-B. Dumas. Milne., Duclert, A.
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Sequence 7 from Patent W00163290
AX331601
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                                                                                                              Thompson,D.A. and Weigel,R.J. hAG-2, the human homologue of the Xenopus laevis cement gland gene XAG-2, is coexpressed with estrogen receptor in breast cancer cell
Submitted (10-JUN-1997) Surgery, Stanford, 1
Building, Room P228, Stanford, CA 94305, USA
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 838)
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Database: N_Geneseq_032802:*
Database sequences: 1736436
Database length: 858457221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search information block:
Query: US-09-674-266A-181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MODEL=frame+_p2n.model -DEV=xlh
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1993-2000
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Compugen Ltd.
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     9 2.2e-51
9 2.3e-51
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6 2.8e-51
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7 6.6e-51
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8.3e-99
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AAZ52865

from:

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156 34 106 100.000

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+ 542.00 1042.94
- 535.00 1040.71
+ 529.00 1028.60
+ 516.00 1003.66
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DT 14-MAR-2000 (first 6
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Pancreas; tumor; EST;
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PF NESCHIAL A, Specht
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XX
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PT Proteins -
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PT Rosenthal A, Specht
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PT New human nucleic ac
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PP Claim 2; Page 188; 5
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Claim 2; Page 188; 5
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Claim 2; Page 188; 5
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CThis invention descr
CC activity. The sequen
CC pancreatic tumor cDN
CC in AAY73814-Y74252.
XX
SQ Sequence 1020 BP; 34
              alignment_scores:
Quality: 1063.00
Patio: 5.160
                                                                                                                                                                                                      This invention describes novel polypeptides and their encoding nucleic acids derived from human pancreatic tumor tissue which have cytostatic activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. AAZ52858-Z53014 represent expressed sequence tag (EST) fragments derived from a human pancreatic tumor cDNA library and which encode the proteins represented
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human prostate tumor cDNA library derived
                                                                                                                                                                                     represent expressed se pancreatic tumor cDNA in AAY73814-Y74252.
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P-PSDB; AAY73835, AA
                                                                                                                                        Sequence 1020 BP; 341
                                                                                                                                                                                                                                                                                                                                                                                                                                        New human nucleic acid sequences from pancreatic tumors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAR-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY73836, AAY73837.
                                                                                                                                                                                                                                                                                                                                                                        502pp; German.
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Length:
Gaps:
Percent Identity:
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C AAC58380;
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DT 29-JAN-2001 (first e
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DT 29-JAN-2001 (first e
XX
DT 29-JAN-2001 (diagnous)
KW Human PRO1030 nucleot
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KW noctropic; neuroprote
KW neuronal disorder; gl
KW hypothalamic disorder;
KW hypothalamic disorder
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Inflammatory disorder
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PD 14-SEP-2000.
XX
O6-JAN-2000; 2000WO-U
XX
O8-MAR-1999; 99WO-U
PR 02-JUN-1999; 99WO-U
PR 02-JUN-1999; 99WO-U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTAAAGAAAGTGTTTGCTGAAAATAAAGAAATCCAGAAATTGGCAGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                         nucleotide sequence SEQ
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99WO-US12252.
99US-0141037.
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alignment_block: US:09-674-266A-181

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AAC58380

Percent Similarity:

Align seg 1/1 to: AAC58380

from:

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920

155

34

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50

15,

204

105

1 56 17

34

17 104

CCGACTCACACAAGGCAGGTGGGGTGAGGAAATCCAGAGTTGCCATGGAGA

ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerAr

AGACTCAGCTGTGCTGGCACACTCAGAAGCTT.GGACCGCATCCTAGCCG

205

rArgProLysLeuProGlnThrLeuSerArgGlyTrpGlyAspGlnLeuI

84

67

254

alignment_scores:

Quality:

Ratio:

1025.00 5.025 99.029

Percent Identity: 98

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CC The present invention describes an isolated antibody that binds to CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO355, CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO3111, PRO1055, PRO11009, PRO1187, PRO1030, PRO1097, PRO1107, PRO1111, PRO1152, PRO1182, PRO1182, PRO1187, PRO1187, PRO1181, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, CC C reatment, diagnosis and prevention of cancer. The antibodies and other CC anti-tumour compounds maybe used to treat various conditions, including CC those characterised by overexpression and/or activation of the amplified CC PRO genes. Exemplary conditions or disorders to be treated with such CC antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, CC (e.g., renal, liver, kidney, kidney, kidney, kidney, kidney, kidney, ki
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26-JUL-1999;
30-NOV-1999;
20-DEC-1999;
05-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thirty PRO polynucleotides encoding treatment, diagnosis and prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 50; Fig 27; 286pp; English.
Sequence 920 BP;
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                                             present invention.
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2000WO-US00219.
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                                                         Claim 3; Page 167; 310pp; German.
                                                                                                          New nucleic acid sequences expressed in ovarian, tissues, and derived polypeptides, for treatment identification of therapeutic agents
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have anticancer activity and are highly expressed in ovarian tumor tissue (and some also in testis and breast cancer tissue). The products of the invention can be used for gene therapy. (A) are used (i) for recombinant expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of ovarian cancer; (ii) directly for treating this form of cancer (including expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling ESTs (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTs from different libraries may represent different
                                                  parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. AAZ77450-Z77572 represent the human ovarian tumor cDNA library derived EST fragments described in the metho of the invention and encode the protein fragments represented in AAY76505-Y76638.
  Sequence 1018
  BP; 343
  Ą.
     212
  Ç;
     216
  G;
  247 T;
0 other;
                                                                                                       the method
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alignment_block: alignment_scores US-09-674-266A-181 x AAZ77486 Percent Similarity: Quality: Ratio: 1018.50 5.017 98.068 Percent Identity: Gaps: 86 207 2

Align seg 1/1 to: AAZ77486 1 ArgLeuSerCysAlaGlyThrLeuSerGlySer.GlyProHisProSerA from: 1 to: 1018 17

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154 104 GCCGACTCACACAAGGCAGGTGGGTGAGGAAATCCAGAGTTGCCATGGAG 34 17 LysIleProValSerAlaPheLeuLeuLeuValAlaLeuSerTyrThrLe rgArgLeuThrGlnGlyArgTrpValArgLysSerArgValAlaMetGlu AAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCCCTCTCCTACACTCT 203 50 153 S S

204

50

uAlaArgAspThrThrValLysProGlyAlaLysLysAspThrLysAspS

GGCCAGAGATACCACAGTCAAACCTGGAGCCAAAAAGGACACAAAGGACT

253 67

404 133 453

This invention describes novel nucleic acid (cDNA) sequences (A) which

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seq_documentation_block:
ID AAV29047 standard; cD
XX AAV29047;
XX 21-AUG-1998 (first e
XX Human protein compris
XX Human protein; secret
KW Human protein;
XX Homo sapiens.
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     Percent Similarity:
                                                                                                                                                                                                                                          This is the nucleotide sequence of a novel human protein comprising a secretory signal isolated from stomach cancer cells. Its proteins can be used as nutritional sources or supplements. The proteins may also have cytokine functions, immune modulating functions, haematopoiesis regulating activity, activin/inhibin regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory
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(SAGA) SAGAMI CHEM RES CENTRE.
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/product= "human protein comprising secretory
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DT 03-SEP-2001 cancer at
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PD 05-APR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps. By inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present
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03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                  erLysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGluCys
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AspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTr 79
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                                                                                                                                                                                                                                                                                                     gValAlaMetGluLysIleProValSerAlaPheLeuLeuLeuValAlaL 46
                                                                     GGGTGACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAAAT
                                                                                         pGlyAspGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLysS
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seq_documentation_block:
ID AAV19155 standard;
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                                         New isolated human XAG growth factor(s) - used to develop for treating e.g. liver, lung or breast diseases or hyperproliferative disorders, e.g. cancer.
                                                                                       WPI; 1998-169093/15
                                                                                                                                                                                                                                                                                                                                                 Human XAG
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This cDNA clone codes for huXAG-1 (see AAW37844), a member of a novel family of human growth factors also including huXAG-2 (see AAW37845)

Claim 5; Fig 1; 141pp; English.

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Colon cancer specific gene (CCSG), provides a molecular marker for CC colon cancer. huXAG-1 cDNA was isolated from a cDNA library CC derived from human colon cancer tissue. Vectors, host cells, and streaming methods for identifying agonists and CC antibodies, and screening methods for identifying agonists and CC antagonists of huXAG-1 are provided. HuXAG polypeptides are growth CC factors and can be used to stimulate proliferation of cells. They CC can be used to stimulate the proliferation and differentiation of CC such as fulminant liver failure caused by cirrhosis, liver damage CC caused by viral hepatitis and toxic substances. They can also be used to stimulate or promote liver regeneration, e.g. after considered by various pathological states. They can be used to stimulate proliferation and differentiation and promote the repair CC simulate proliferation and differentiation and promote the repair CC creat acute or chronic lung damage, e.g. emphysema, which results considered to the bronchiolar epithelium to prevent, attenuate, or creat acute or chronic lung damage, e.g. emphysema, which results considered to promote healing of breast tissue and could therefore be used to promote healing of breast tissue considered to promote healing of breast tissue and could therefore be used to promote healing of breast tissue considered to promote the proliferative disorders, including cancer, in colon cancer. The products can also be used for colon cancer. The products can also be used for detection and collaboration cancer, in the properties of the products can also be used for detection and collaboration cancer. The products can also be used for detection and collaboration cancer. The products can also be used for detection and collaboration cancer. The products can also be used for detection and collaboration cancer. The products can also be used for detection and collaboration cancer.
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                       ProHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleG1 129
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CCACACAGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAATAAAGAAATCCA
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seq_documentation_block:
ID AAF63314 standard; cl
XX AAF63314;
XX AAF63314;
XX AAF63314;
XX DT 04-MAY-2001 (first (
XX Human huxAG-1/CCSG co
XX Human; growth factor
KW cell proliferation;
KW hepatitis; cancer; co
XX Homo sapiens.
XX US6171816-B1.
XX US6171816-B1.
XX 22-AUG-1996; 96US-
PR 22-AUG-1997; 97US-
XX 23-AUG-1997; 97US-
XX 23-AUG-1996; 96US-
PR 23-AUG-1997; 97US-
XX PF 22-AUG-1997; 97US-
XX NOWEL HUMAN GENOME
XX WPI; 2001-136872/14
DR P-PSDB; AAB72203.
XX Novel human growth :
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XX Novel human growth :
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CC Rhown as a colon cancer specific gene (CCSG). HuxAG-1 sliver factor polypeptide huxAG-1 also CC known as a growth factor. The HuxAG-1 protein is useful for CC identifying compounds capable of enhancing or inhibiting cellular CC response induced by huxAG-1. The protein is also useful for CC proliferation of cells e.g. colon, breast, liver and lung cells, and CC pathologies such as fulminant liver failure caused by cirrhosis, liver CC damage caused by viral hepatitis and toxic substances, for preventing and CC treating damage to the lungs caused by various pathological states and CC cancer. HuxAG-1 and the identified antagonist are useful for treating cancer of cancer in particular colon cancer. Detecting altered levels of huxAG-1 and its polynucleotides are useful for diagnosing or detecting cancer in mammals. The gene encoding huxAG-1 is useful for monitoring human Novel human growth factor polypeptide useful for diagnosing and treating colon cancer and liver diseases, to prevent and heal damage to the lungs and for identifying modulators of therapeutic use . Claim 45; Fig 1; 59pp; (HUMA-) HUMAN GENOME SCI INC Ebner R, English. Endress GA;

96US-0024347 97US-0916576

SSSSS

Sequence

875

BP;

283

A; 189

C; 180

G;

223 T;

0 other;

colorectal chromosome huxAG-1.

carcinoma. huXAG-1 nucleic acid molecules are also useful for identification. The present sequence represents cDNA encoding

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seq_documentation_block:
ID AAV59320 standard; ct
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AC AAV59320;
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                                               109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated mucous-associated polypeptide, zsig10 - used to develop products for treating e.g. tumour metastasis, microbial infections, cystic fibrosis, asthma, bronchitis or inflammatory bowel disease
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                                                                                                                                                                                                                                                                                                                                  Sequence 881
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lAlaMetGluLysIleProValSerAlaPheLeuLeuLeuValAlaLeuS
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seq_documentation_block:
ID AAF44884 standard; cI
XX AAF44884;
XX DT 28-MAR-2001 (first 6
XX DT 28-MAR-2001 (first 6
XX DT 28-MAR-2001 (first 6
XX Human breast cancer;
XX Human; breast cancer;
XX Human; breast cancer;
XX Homo sapiens.
XX WO200078960-A2.
XX PF 23-JUN-2000; 2000WO-1
XX PF 23-JUN-1999; 99US-1
XX PF 23-JUN-1999; 99US-1
XX PF 12-OCT-1999; 99US-1
XX CORI-) CORIXA CORP.
XX PF 23-JUN-1999; 99US-1
XX PF 23-JUN-1999; 99US-1
XX PF 23-JUN-1999; 99US-1
XX PF 23-JUN-1999; 99US-1
XX CORI-) CORIXA CORP.
XX PF 23-JUN-1999; 99US-1
XX CORI-) CORIXA CORP.
XX PF 23-JUN-1999; 99US-1
XX CORI-) CORIXA CORP.
XX PF 23-JUN-1999; 99US-1
XX The prevention, treatmen
XX Claim 25; Page 132;
XX The present inventio
CC The present inventio
CC The present inventio
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CC against, diagnosis o
CC cancer.
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                                     The present invention provides the coding sequences for a number of breast cancer related proteins. These can be used in vaccinations against, diagnosis of and treatment of cancer, particularly breast
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                                                                                                     Claim 25; Page 132; 165pp; English.
                                                                                                                                      New polynucleotides encoding breast tumor specific proteins, useful for prevention, treatment and diagnosis of breast cancer -
                                                                                                                                                                                                                                                                                                                                           23-JUN-2000; 2000WO-US17536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human breast cancer related protein coding sequence SEQ
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seq_documentation_block:
ID AAZ40803 standard; DN
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KW Secreted protein; fine
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PR 04-SEP-1998; 98US-0
PR 13-APR-1998; 98US-0
PR 11-AUG-1998; 98US-0
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                                                                                  117
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                                                               aLeuLysLysValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluG
lnPheValLeuLeuAsnLeuValTyrGluThrThrAspLysHisLeuSer
                                                                                                                      AAACCCTTGATGATTATTCATCACTTGGATGADTGCCCACACAGTCAAGC
                                                                                                                                                         LysProLeuMetIleIleHisHisLeuAspGluCysProHisSerGlnAl
                                                                                                                                                                                                  TCTGGACACARACATATGAARAARCTCTATWTAAATCCAARACAAGCAAC
                                                                                                                                                                                                                         TCGACCCAAACTGCCCCAGACCCTCTCCAGAGGTTGGGGTGACCAACTCA
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                                           TTTAAAAAAKTGTTTGCTGAAAATAAARAATCCAGAAATTGGCARANC
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seq_documentation_block:
ID AAS13480 standard;
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                                                              Claim
                                                                                       Diagnosing, preventing
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                                                                                                                                                                                                                                                                 mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                   vaccine; chromosome
                                                                                                                                                                                                                                                                                                                                                                             metastasis; cytostatic.;
                                                                                                                                                                                                                                                                                                                                                                                   Breast cancer cell membrane protein 7;
                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding breast cancer cell membrane
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                                                                                                                                                       (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
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                                                                              membrane protein
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                                                             62pp; English
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BCMP
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                                                                                         breast cancer
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The invention describes the novel use of a protein found in breast cancer cell membranes (BCMP 7) for diagnosing, preventing and treating breast cancers. The peptide has cytostatic action and potential uses in gene therapy and in vaccines. The polypeptide, antisense nucleic acids, or fusion proteins comprising and Green Fluorescent protein or the DsRe Fluorescent protein, antibodies specific for and/or nucleic acid are

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seq_documentation_block:
ID     AAV29048 standard; ct
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AC      AAV29048;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGly
                                                                                                                                              GAAGAAAGCTCTCAAGTTGCTGAAGACTGAATTG
                                                                                                                                                                                                            CGTCTCTATGCTTACGAACCTGCAGATACAGCTCTGTTGCTTGACAACAT
                                                                                                                                                                                                                           ArgLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMe 195
                                                                                                                                                                                                                                                                                                                                         TGACAAACACCTTTCTCCTGATGGCCAGTATGTCCCCAGGATTATGTTTG
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                                                                                                             /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV29048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the nucleotide sequence of the open reading frame of a novel human protein comprising a secretory signal (AAV3047), isolated from stomach cancer cells. Its proteins can be used as nutritional sources or supplements. The proteins may also have cytokine functions, immune modulating functions, haematopoiesis regulating activity, activin/inhibin regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PROT-)
(SAGA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human proteins with secretory signal sequences - used to tre-
immune deficiencies, infections, tumours, and haematopoietic
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cancer. The polypeptides and monoclonal antibodies specific for t polypeptides can also be used to inhibit the development of lung Agents which bind the polypeptides can be used for detecting lung and for monitoring the progression of lung cancer.

lung cancer

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 The invention provides isolated human lung tumor nucleic acids and polypeptides. The polypeptides can be used for the treatment of lung cancer. The polypeptides and polypucleotides can be used to stimulate cells or antigen presenting cells for use in the treatment of lung
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                                                Claim 1; Page 90; 148pp; English
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98US-0123912.
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                      documentation_block: AAC65817 standard;
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21-FEB-2001

(first entry)

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17-DEC-1999;
30-DEC-1999;
10-JAN-2000;
22-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polypuncleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit development of cancer.
152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated polypeptide comprising an immunogenic portion of a lung protein is used for detecting and monitoring progression of lung
                                                                                                                                                                                                                                                                                                                                   Sequence 793 BP;
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vaccine; detection; ss.
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-DB=Issued_Patents_NA -QFMT=fastap_SUFFIX=PQn.rni
-GAPOP=12_000 -GAPEXT=4_000 -MINMATCH=0_1100 -LOOPCL=0_000
-LOOPEXT=0_000 -QGAPOP=4.500 -QGAPEXT=0_050 -XGAPOP=10_000
-XGAPEXT=0_500 -FGAPOP=6_000 -FGAPEXT=7_0.00 -YGAPOP=10_000
-YGAPEXT=0_500 -FELOP=6_000 -FERAFEXT=7_000 -START=1
-MATRIX=blosum62 -TRANS=human40_cdi -LIST=45 -DCCALIGN=200
-THR_SCORE-PCt -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pfs -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US09674265_@CGN1_1_46 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
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MB. seq: US-08-916-576B-35+ 6
MB. seq: US-08-916-576B-36+ 44
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MB. seq: US-08-916-576B-36+ 22
MB. seq: US-08-916-576B-38+ 11
MB. seq: US-08-916-576B-38+ 11
MB. seq: US-08-916-576B-14+ 11
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    US-08-916-576B-1
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seq_documentation_block:
; Sequence 1, Application
; Patent No. 6171816
alignment_block:
US-09-674-266A-181 x US-08-916-576B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: STEFFE, ERIC K.

REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1486
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 23-AUG-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1100 NEW 1
CITY: WASHINGTON
STATE: DC
COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20005-3934
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131..595
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Percent Identity:
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GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAs
FILE REFERENCE: GENSET: 021A
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-07-09
EARLIER FILING DATE: 1998-08-16
EARLIER FILING DATE: 1998-08-16
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
SEQ ID NO 61
LENGTH: 1689
                                                                                                                                                                                                                                                                                                  seq_documentation_block:
   Sequence 61, Application US/09247155A
   Patent No. 6312922
                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-247-155-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nLysLeuAlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrThrA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCACACAGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAATAAAGAAATCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spLysHisLeuSerProAspGlyGlnTyrValProArgIleMetPheVal 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAATTGGCAGAGCAGTTTGTCCTCCTCAATCTGGTTTATGAAACAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnAr 179
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alignment_scores:
    Quality:
    Ratio:
Percent Similarity:
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; LOCATION: 1674..1689
US-09-247-155-61
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NAME/KEY: sig_peptide

LOCATION: 51..110

OTHER INFORMATION: Von Heijne matrix

OTHER INFORMATION: score 11.2

OTHER INFORMATION: seq aflllvalsytla/RD
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NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                        178
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CCCTCTCCTACACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAA
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                                                          ValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAs
                                                                                             CTGACAAACACCTTTCTCCTGATGGCCAGTATGTCCCCAGGATTATGTTT
                                                                                                        hrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMetPhe
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alignment_scores:
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US-09-674-266A-181 x US-09-247-155-149
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APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAS
FILE REFERENCE: GENSET.021A
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,273
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
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                                                                                                                                                                                                                                  Align seg 1/1 to: US-09-247-155-149
                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patent.pm
SEQ ID NO 149
LENGTH: 940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 149, Application US/09247155A Patent No. 6312922
                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: n=a, g, -09-247-155-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 11.1999998092651
OTHER INFORMATION: seq AFLLLVALSYTLA/RD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 177..569
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LOCATION: 482
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LOCATION: 177..236
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gArgLeuThrGlnGlyArgTrpValArgLysSerArgValAlaMetGluL
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931..939
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; Sequence 78, Application US/0904(
; Patent No. 6210883
; GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Wang, TongTong
TITLE OF INVENTION: COMPOUNDS
TITLE OF INVENTION: OF LUNG (
NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-040-984-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           534
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                                                                                                       APPLICATION NUMBER: FILING DATE: 18-MAF CLASSIFICATION:
                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 98104
                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                  Diskette
                                                                                                                           18-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                         COMPÓUNDS AND METHODS FOR DIAGNOSIS
OF LUNG CANCER
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SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLLOGY: linear
US-09-040-984-78
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seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-123-912-78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-674-266A-181 x US-09-040-984-78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
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                                               ysAlaLeuLysLeuLeuLys 203
                                                                                            CTATGCTTACAAACT.GCAGATACGCTCTGTTGCTTGACACAT...GAAA
                                                                                                            uTyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysL 197
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seq_documentation_block:
; Sequence 78, Applicati

Application US/09123912A

Percent Similarity:

Ratio:

Gaps: Percent Identity:

93.684

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; OTHER INFORMATION: Where n
; NAME/KEY: modified_base
; LOCATION: (765)
; OTHER INFORMATION: Where n
; NAME/KEY: modified_base
; LOCATION: (787)
; OTHER INFORMATION: Where n
US-09-123-912-78
                                 alignment_scores:
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SEQ ID NO 78
LENGTH: 793
TYPE: DNA
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GENERAL INFORMATION:
                                                                                                                                                                                      NAME/KEY: modified_base
LOCATION: (732)
OTHER INFORMATION: where n
NAME/KEY: modified_base
LOCATION: (740)
OTHER INFORMATION: where n
NAME/KEY: modified_base
LOCATION: (748)
OTHER INFORMATION: where n
NAME/KEY: modified_base
LOCATION: (748)
OTHER INFORMATION: where n
NAME/KEY: modified_base
LOCATION: (758)
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NAME/KEY: modified_base
LOCATION: (660)
OTHER INFORMATION: Where n
NAME/KEY: modified_base
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APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS AND METHODS
FILE REFERENCE: 210121.455C1
CURRENT APPLICATION NUMBER: US/09/123,912A
CURRENT FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                              LOCATION: (710)
OTHER INFORMATION: Where n
NAME/KEY: modified_base
LOCATION: (711)
OTHER INFORMATION: Where n
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PRIOR FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 114
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OTHER INFORMATION: Where n
NAME/KEY: modified_base
LOCATION: (492)
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OTHER INFORMATION: Where
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                      Quality:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: XU, Jiangchun
TITLE OF INVENTION: COMPOUNDS AND METHODS FOI
TITLE OF INVENTION: OF COLLON CANCER
FILE REFERENCE: 210121.471
CURRENT APPLICATION NUMBER: US/09/221,298
CURRENT FILING DATE: 1998-12-23
CURRENT FILING DATE: 1998-12-23
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 32
LENGTH: 401
TYPE: DNA
ORGANISM: Human
US-09-221-298-32
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; Sequence 32, Applicati
; Patent No. 6284241
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US-09-674-266A-181 x US-09-123-912-78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTGGCAGAGCAGTTTGTCCTCCTCAATCTGGTTTATGAAACAACTGACA 401
                                                                                                                                                                                                                                   Application US/09221298
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alignment_block:
US-09-674-266A-181 x US-09-221-298-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 35, Application Patent No. 6171816
                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                       APPLICANT: YU, GÜO-LIANG
APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
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                                                                   CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   352 CTGGAAGATATTCAAACCGTCTCTATGCTTACGAACCTGCAGATACAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 LysProGlyAlaLysLysAspThrLysAspSerArgProLysLeuProGl
                                                                                                                                                                                  STATE: DC
COUNTRY: US
ZIP: 20005-3934
                                                                                                                                                                                                                                      STREET: 1100 NEW CITY: WASHINGTON
                                                     FILING DATE:
                                                                                                                                                                                                                                                        ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L. STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProArgIleMetPheValAspProSerLeuThrValArgAla.AspIleT
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   US 60/024,347
                                                                     US/08/916,576B
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Percent Identity:
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23-AUG-1996

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seq_documentation_block:
   Sequence 5, Application US/08916576B
   Patent No. 6171816
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Quality:
Ratio:
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; MOLECULE TYPE:

US-08-916-576B-35
                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-916-576B-5
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REGISTRATION NUMBER: 36,688
REFERENCE,DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 386 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-08-916-576B-35 from: 1
                                                                             GENERAL INFORMATION:
APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
                                      APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
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NAME: STEFFE, ERIC K.
CORRESPONDENCE ADDRESS:
                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201
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                                                                                                                                                                                                                                                                                                                                                                                                PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSe 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uIleGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeuValTyrGluT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAATCGTCTCTATGCTTACGAACCTGCAGATACA
                                                                                                                                                                                                                                                                                                                                  rAsnArgLeuTyrAlaTyrGluProAlaAspThr 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAACTGACAAACACCTTTCTCCTGATGGCCAGTATGTCCCCAGGATTATG
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; LOCATION:
; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-916-576B-5
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TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 732 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                        US-09-674-266A-181 x US-08-916-576B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                107 sHisLeuAspGluCysProHisSerGlnAlaLeuLysLysValPheAlaG
                                                                                                                                        196 GAAGGTCTCTTTATGCTCAAAAAAGTAAGAAGCCATTAATGGTTATTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                  91 GluAlaLeuTyrLysSerLysThrSerAsnLysProLeuMetIleIleHi 107
                                                                                                                                                          74 hrLeuSerArgGlyTrpGlyAspGlnLeuIleTrpThrGlnThrTyrGlu
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                                                                                                                                                                                                                                                                                                               41 LeuLeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLy
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/916,576B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1100 NEW CITY: WASHINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                 sProGlyAlaLysLysAspThrLysAspSerArgProLysLeuProGlnT 74
CTCTTACTCGTCACAGTTTCTTCCAACCTTGCC....ATTGCAATAAA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
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Percent Identity: 64.671
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; MOLECULE TYPE: US-08-916-576B-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3
                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                   TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 base pairs
                                                                                                                                                      REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396
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                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & STREET: 1100 NEW YORK AVENUE, SUITE 600
                                   TOPOLOGY:
                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProArgIleMetPheValAspProSerLeuThrValArgAlaAspIleT 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuLeuLeuAspAsnMetLysLysAlaLeuLysLeuLeuLysThrGluLe 206
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6171816
                                                                  nucleic acid
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                                                  single
                                                                                                                                       371-2540
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                                                                                                                                                                                           1488.0500001
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alignment_block: us-09-674-266A-181 \times us-08-916-576B-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/08916576B Patent No. 6171816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: YU, GU
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: DILLON, FRANCE
APPLICANT: EBHER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
APPLICANT: NOVEL HUMAN GROWTH FACTORS
                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6(
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 CTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAAAAAGGACACAAAG
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                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                         CITY: WASHINGTON STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                        COUNTRY:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerAsnLysProLeuMetIleIleHisHisLeu.AspGluCysProHisS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAAATCCAAGACAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThr.
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4.643
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                                                                                      US 60/024,347
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1488.0500001
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Gaps:
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seq_documentation_block:
; Sequence 10, Application US/08916576B
; Patent No. 6171816
; GENERAL INFORMATION:
; APPLICANT: YU, GUO-LIANG
; APPLICANT: EBUER, REINHARD
; APPLICANT: EBUER, REINHARD
; APPLICANT: ENDRESS, GREGORY A.
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US-09-674-266A-181 x US-08-916-576B-9
                                                                                                                                                                      seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-916-576B-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110
                                                                                                                                                                                                                                                                                     371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysGluIleGlnLysLeu......AlaGluGlnPheVa 136
                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTGAGTGCCCACACAGTTCAAAGTTTTTAAAGAAAGTGTTTNGC.....
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                                                                                                                                                                                                           NTGGNCNATTTTTCCCCCGGNTTTTTTTTTTTTGGCCCC
                                                                                                                                                                                                                                              pGlyGlnTyrValProArgIleMetPheValAspPro 164
                                                                                                                                                                                                                                                                                     NCCCCNTNAATTTGGGTTTTGGAAACAATGGGCAAACACCTTTTTTGTTG
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3.728
74.096
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Percent Identity: 70.482
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 506 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6(
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,576B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                           214
                                                                                                                                                                         146 pLysHisLeuSerProAspGlyGlnTyrValProArgIleMetPheValA 163
                                                                                                                                                                                                                                                                                                                                     113 OHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGlnL 130
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MEDIUM TYPE: Floppy disk
                                                                                                                                                         164
                                                                                                                                                                                                                                     114
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                                                                                                                                                                                                                                                                                                              64 ACACAGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAATAAAGAAATCCAGA
                                                                                                                                                                                                                                                                                                                                                                                              14 AAGACAAGCAACCAAACCCTTGATGATTATTCATCANTTGGATGAGTGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                97 LysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGluCysPr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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                                                                       ysLeuAlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrThr.As
                                  nArgLeuTyrAlaTyr 183
                                                                                                                                                       CAAACACCTTTCTCCTGATGGCCAGTATGTNCCCAGGGTTATGTTTGTTG
                                                                                                                                                                                                                                     AATTGGCAGAGCAGTTTGTCCTCCTCAATCTGGTTTATGAAACAACTGGA
CGTNNCTTATGCTTAC
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Ratio:
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87.778
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                                                                                                                                                         213
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seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-916-576B-37

seq_documentation_block:

Sequence 37, Application US/08916576B Patent No. 6171816

YU, GUO-LIANG

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alignment_block:
US-09-674-266A-181 x US-08-916-576B-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-916-576B-37
                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-08-916-576B-37 from: 1 to: 158
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APPLICANT: YU, GUO
APPLICANT: DILLON,
APPLICANT: EBNER,
APPLICANT: ENDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/916,576B FILING DATE: CLASSIFICATION: 536
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
CORRESPONDENCE STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 158 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: li
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APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
156
                                                                         106
                                    65
                                                                                                               48
                                                                                                                                                      56
                                                                                                                                                                        31 aMetGluLysIleProValSerAlaPheLeuLeuLeuValAlaLeuSerT 48
                                                                                                                                                                                                                                                      15 ProSerArgArgLeuThrGlnGlyArgTrpValArgLysSerArgValAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                         AAG 158
                                    Lys 65
                                                                                                               yrThrLeuAlaArgAspThrThrValLysProGlyAlaLysLysAspThr 64
                                                                                                                                                      CATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCCCTCTCCT 105
                                                                                                                                                                                                                               CCTAGCCGCCGACTCACACAAGGCAGGTGGGTGAGGAAATCCAGAGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : (202) 371-2600
(202) 371-2540
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alignment_block:
US-09-674-266A-181 x US-09-030-607-209
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seq_documentation_block:
; Sequence 209, Application US/09439313
                                                                 seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-439-313-209
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FER-1000
CLASSIFTONE: 25-FER-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 2101

TELECOMMUNICATION INFORMATION: (206) 622-4900

TELEPHONE: (206) 682-6031

INFORMATION FOR SEQ ID NO: 209:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-09-030-607-209 from: 1
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Patent No. 6262245
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUN
NUMBER OF SEQUENCES: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
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                                                                                                              153
                                                                                                                                                                                                 103 CTGGAGCCAAAAAGGACACAAAGGACTCTCGACCCAAACTGCCCCAGACC 152
                                                                                                                                                                                                                          58 roGlyAlaLysLysAspThrLysAspSerArgProLysLeuProGlnThr 74
                                                                                                                                                                                                                                                                                                            41 uLeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLysP
                                                                                                                                                                                                                                                                                                                                                                                               25 ValArgLysSerArgValAlaMetGluLysIleProValSerAlaPheLe
                                                                                                                                                       75 LeuSer 76
                                                                                                                                                                                                                                                                                     53 GCTCCTTGTGGCCCTCTCCTACACTCTGGCCAGAGATACCACAGTCAAAC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 159 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                           3 GTGAGGAAATCCAGAGTTGCCATGGAGAAAATTCCAGTGTCAGCATTCTT 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity:
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NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 209
LENGTH: 159
TYPE: DNA
ORGANISM: Homo sapien
US-09-439-313-209
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US-09-674-266A-181 x US-09-439-313-209
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                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                     Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Day, Craig
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
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                                                          APPLICANT: EBNER, KELMING.
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX,
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Xu, Jiangchun
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APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                         153 CTCTCC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 CTGGAGCCAAAAAGGACACAAAGGACTCTCGACCCAAACTGCCCCAGACC
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                  COUNTRY: US
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GTGAGGAAATCCAGAGTTGCCATGGAGAAAATTCCAGTGTCAGCATTCTT
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Reed, Steven G.
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Fanger, Gary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dillon, Davin C.
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                                                                                                                     KESSLER, GOLDSTEIN & FOX, P.L.L.C.
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Percent Identity:
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alignment_block: us-09-674-266A-181 \times us-08-916-576B-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/024
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                191 GAGATCATATTCATTGG...AGGACACTGGAAGATGGGAAGAAAGAAGCA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
145 ThrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMetPh
                                                                                                                                                                                                                                                                                                                                                           141 GCTCCTCGTCATCTCTGATGGACATAATGGGCTTGGAAAGGGTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: cDNA
                                                                                           130 ysLeuAlaGluGlnPheValLeuLeuAsnLeu.....ValTyrGluThr 144
                                                                                                                                288 AGCTTGCAAAGCTCTAAAGCCCAAATTTGCAGAATCTACGGAAATTTCAG
                                                                                                                                                                                                                                       97 LysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGluCysPr 113
                                                                                                                                                                                                                                                                                                                     80 lyAspGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                     91 GAGACGCGGCCTCGTCTCGGGGCCACCTGTTTGCTGGGCTTCAGTTTCCT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 AspSerArgProLysLeuProGlnThr.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: doub
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                                                        AACTCTCCCATAATTTTGTTATGGTAAATCTTGAGGATGAAGAGGAACCC
                                                                                                                                                               OHISSERGINALALEULYSLYSVALPheAlaGluAsnLysGluIleGlnL 130
                                                                                                                                                                                                        GCTGCCAGTGGACTGCCCCTGATGGTGATTATTCATAAATCCTGGTGTGG
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gb_est2:BG179160
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Search time (sec): 1720.980000
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Query length:
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gb_est2:BE867131
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                                                                                                                                                    gb_est2:BF680021
                                                                                                                                                                    gb_est1:AA314225
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-QGAPEXT-0.050 -XGAPOP=10.000 -XGAPEXT-0.050 -FGAPOP-6.000
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-MINLEN-0 -MAXLEN-200000000 -USER-US09674266_eCGN1_12564
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-NO_XLPXY -WAIT -THREADS-1
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SOURCE
ORGANISM
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ORIGIN
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Ratio: 5.169
Percent Similarity: 100.000
                                                                                                              US-09-674-266A-181 x BG778248
                                                                                   Align seg 1/1 to:
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TITLE
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                                                         12
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BG778248 from: 1

to: 666

61

Gaps: 0
Percent Identity: 100.000

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LOCUS BG778248
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Location/Qualifiers
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BG778248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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/note="Organ: prostate; Site_2: Sit1 (ggccattatggcc);
/note="Organ: prostate; Site_2: Sit1 (ggccattatggcc);
/note="Organ: prostate; Site_2: Site_
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/clone_lib="NIH_MGC_60"
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7 Mus musculus 10 day
03 602831911F1 NCI_CGA
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SOURCE
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LOCUS AW582256
                                                                                                                                                                                                                                                                                                                       KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                        gb_est1:AW582256
                                                                                                                                          HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01
                            Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2=QV4-ST0212-
120100-075-e10&t3=2000-01-12&t4=1)
                 Seq
                                                                                                     Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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              primer: puc 18 forward
  quality
 sequence stop: 687
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Primates;
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0 ST0212
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Ratio: 5.169
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/clone_lib="ST0212"
/dev stacc-".
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VERSION
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                                                                                                                                                                                                                                                                                                                       Quality: 1002.00
Ratio: 5.165
Percent Similarity: 100.000
                                                                                                                                                                                                                             Align seg 1/1 to: BI523582
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 102
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TCTCCTACACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAAAAG
                 euSerTyrThrLeuAlaArgAspThrThrValLysProGlyAlaLysLys 62
                                                                           AGTTGCCATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCC
                                                                                             gValAlaMetGluLysIleProValSerAlaPheLeuLeuLeuLeuValAlaL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAAGAAAGCTCTCAAGTTGCTGAAGACTGAATTG
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http://image.llnl.gov
Plate: LLAM11504 row: h column: 04
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1 (bases 1 to 624)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               190
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-*Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: ECORV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NHH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5201331"
/clone_lib="NIH_MGC_122"
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAATTGGCAGAGCAGTTTGTCCTCCTCAATCTGGTTTATGAAACAACTG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              erLysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGluCys 112
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                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAMI0186 row: o column: 08 High quality sequence stop: 732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 750)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections of the collection of the colle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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EST.
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BG179160
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                                                                                                                                                                                                                                                                                         quality sequence stop:
Location/Qualifiers
/clone="IMAGE:4431583"
/clone_lib="NIH_MGC_91"
/tissue_type="adenocarcinoma, cell
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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.M.A.G.E. Consortium
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seq_documentation_block:
LOCUS BE748141
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ORIGIN
                                                                        seq_name: gb_est2:BE748141
                 DEFINITION
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Ratio: 5.147
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 ProSerArgArgLeuThrGlnGlyArgTrpValArgLysSerArgValAl
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                                                                                                                                                                                                                                                                                                                                                    laLeuLysLeuLeuLysThrGlu 205
                                                                                                                                                                                   rAlaTyrGluProAlaAspThrAlaLeuLeuAspAsnMetLysLysA 198
                                                                                                                                                                                                                                               SerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeuTy 181
                                                                                                                                                                                                                                                                                                          LysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGlyAs 81
                                                                                                                                                                    TGCTTACGAACCTGCAGATACAGCTCTGTTGCTTGACAACATGAAGAAAG
                                                                                                                                                                                                                               TCTCTGACAGTTAGAGCCGATATCACTGGAAGATATTCAAATCGTCTCTA
                                                                                                                                                                                                                                                                                           AAGGACTCTCGACCCAAACTGCCCCAGACCCTCTCCAGAGGTTGGGGTGA
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                                                                                                        CTCTCAAGTTGCTGAAGACTGAA 587
               601571509F1 NIH_MGC_55 Homo sapiens
mRNA sequence
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Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 174 c 158 g 183 t 1 others
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                              9d 689
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Gaps:
                                 mRNA
               cDNA clone IMAGE:3838347 5',
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                               linear
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                               EST 15-SEP-2000
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REFERENCE
AUTHORS
TITLE
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KEYWORDS
SOURCE
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US-09-674-266A-181 x BE748141
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Percent Similarity:
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                                                                       153
                                                                  15 ProSerArgArgLeuThrGlnGlyArgTrpValArgLysSerArgValAl
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pGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLysSerLysT
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
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BE748141.1 GI:10162133
EST.
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Plate: LLCM525 row: a column: 04
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NIH_MGC_55"
/clone_lib="NIH_MGC_55"
/tissue_type="from acute myelogenous leukemia"
/lab_host="DH10B (TI phage-resistant)"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattaggcc);
Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattaggcc);
Double-stranded cDNR was prepared from cell line RNA.
); bouble-stranded cDNR was prepared from cell line SNA.
); bouble-stranded cDNR was prepared from cell line SNA.
); and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGACAGCGCCGACATG-dT(30)BN-3'
(where B = A, C, Or G and N = A, C, G, Or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.131
100.000
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Gaps: 0
Percent Identity: 99.476
                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 689
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REFERENCE
AUTHORS
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VERSION
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ORIGIN
                 BASE COUNT
                                                                                                                                                                  FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAGAGCAGTTTGTCCTCCTCAATCTGGTTTATGAAACAACTGACAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAATAAAGAAATCCAGAAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          755 bp mRNA linear EST039 Human hepatocellular carcinoma subtracted c sapiens cDNA clone P39 5', mRNA sequence.
                                                                                                                                                                                                                   Email: wuling_z@hotmail.com
Human hepatocellular carcinoma cDNA research supported by Institute
of Digestive Disease, Henan Medical University; cDNA insert
sequencing: Genetech Biotechnology Company Limited. cDNA library
construction: Department of Nucleic Acid Research, Institute of
                                                                                                                                                                                                                                                                                                               2 Jingba Road, Zhengzhou, 450003, Henan Province, Tel: 86 0371 3921444
Fax: 86 0371 6960571
                                                                                                                                                                                                                                                                                                                                                                      Contact: Wuling Zhu
Department of Nucleic Acid Research
Institute of Digestive Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhu, W., Duan, F., Liu, D., Ma, J., Bai, J. and Gao, T. Suppression subtracted hybridization to identify differentially expressed genes of hepatocellular carcinoma and expressed sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
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                 237
                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="p39"
                               /note="Organ:
                                                      library
                                                                      /clone_lib="Human hepatocellular
                                                                                                                                                                ocation/Qualifiers
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               : Liver"
158 g
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               189
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                                                                      carcinoma
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ACCESSION
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                        isLeuSerProAspGlyGlnTyrValProArgIleMetPheValAspPro 164
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                                                                                                                                                                                                        CTCTCAAGTTGCTGAAGACTGAATTG
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Homo sapiens
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
1 (bases 1 to 740)
                                                                                               mRNA sequence.
BG501149
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCTCTCCTACACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAlaLys 61
CysProHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIl 128
                                                                                                                              ysSerLysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGlu 111
                                                                                                                                                                                                                                           TTGGGGTGACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATA 263
                                                                                                                                                                                                                                                                                 yTrpGlyAspGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrL 95
                                                                                                                                                                                                                                                                                                                                                                                                       AAGGACACAAAGGACTCTCGACCCAAACTGCCCCAGACCCTCTCCAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATCCAAGACAAGCAACAAACCCTTGATGATTATTCATCACTTGGATGAG 313
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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/Clone=lib="NIH_MGC_60"
/tissue_type="adenocationoma"
/lab_host="DH10B (T] phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
/note="Organ: postate; Vector: pDNR-LIB (Clontech);
/note="Organ: pDNR-LIB (Clontech);
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171 c
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/db_xref="taxon:9606"
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 788)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can
                       248
                                                                                                                                                                                                                                                                                                                                                                                                          quality sequence stop:
Location/Qualifiers
              /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5202866"
/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
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alignment_scores:

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VERSION
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ACCESSION
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LOCUS AW956284
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 721)

Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Hol, L., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
                                                                                     EST.
                                                                                                                      EST368354 MAGE resequences,
                                                              Homo sapiens
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alignment_scores:
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gLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetL
                                        erLysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGluCys 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assessment of gene expression patterns in a model of metastasis using a 19,200 element cDNA microarray Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
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Plate: 90
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/db_xref="taxon:9606"
/clone_lib="MAGE resequences, |
/note="Vector: pBluescriptSKm"
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                                                                                                                                                         14 HisProSer...ArgArgLeuThrGlnGlyArgTrpValArgLysSerAr
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                                                                                      gValAlaMetGluLysIleProValSerAlaPheLeuLeuLeuValAlaL 46
                                                                                                                                       CACGCGTCCGGCCGGCCGACTCACACAAGGCAGGTGGGGTGAGGAAATCCAG
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TCTCCTACACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAAAAG
                                                                   AGTTGCCATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCC
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                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10467 row: i column: 18
High quality sequence stop: 750.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 866)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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602409569F1 NIH_MGC_91 Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: No:
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies
Note: this is a NIH_MGC Library."
a 194 c 189 g 212 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:4539353"
/clone_lib="NIH_MGC_91"
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Gaps:
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seq_name: gb_est2:BM129777
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                                                                                                                                                                                                                                                                                                                                                                               Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.
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                Library was constructed by Dr. Douglas Melton DNA sequencing by Washington University Genome Sequencing Center For information obtaining a clone please contact: Juliana Brown
                                                                                                                             Tel: 617-495-1812
Fax: 617-495-8557
                                                                                                                                                                                                        Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity
                                                                                                                                                                                                                                                                                   Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi
                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Other_ESTs: if23a08.x1
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                                                                                                    Email: dmelton@biohp.harvard.edu
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(brown@fas.harvard.edu)
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                                                                                                nPheValLeuLeuAsnLeuValTyrGluThrThrAspLysHisLeuSerP 151
                                                                                                                                                                                 LeuLysLysValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGl 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ArgLeuThrGlnGlyArgTrpValArgLysSerArgValAlaMetGluLy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D
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140 c
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/dev_stage="Adult"
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/db_xref="taxon:9606"
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Tissue Procurement: DCTD/DTP
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, M
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/clone=lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
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/cell_line="MGC3"
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National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                            602612442F1 NIH_MGC_60 Homo sapiens
http://image.llnl.gov
Plate: LLCM1606 row: d column: 12
High quality sequence stop: 812.
                                           CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TGCCCACACAGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAATAAAGAAAT
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Ratio:
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/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
/note="Organ: prostate; Vector: pDNR-LIB (ggccattatggcc); Site_1: SfiI (ggccgctcggcc); Site_2: SfiI (ggccattatggcc);
Site_1: SfiI (ggccgctcggcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA.
); Double-stranded cDNA was prepared from cell line RNA.
); daptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATTCTAGAGGCCGACATATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGGCGGCCACATG-dT(30)BN-3'
(where B = A, C, Or G and N = A, C, G, Or T). Average
insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratorles (Palo Alto, CA). Note: this is a NIH_MGC
Library."
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/clone_lib="NIH_MGC_60"
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                             hrThrValLysProGlyAlaLysLysAspThrLysAspSerArgProLys
                                                                                      GTCAGCATTCTTGCTCCTTGTGGCCCTCTCCTACACTCTGGCCAGAGATA 10:
                                                                                                                                                                                                  CAAGGCAGGTGGGTGAGGAAATCCAGAGTTGCCATGGAGAAAATTCCAGT 51
gb_est2:BE870718
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 734)
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Plate: LLAM9574 row: 1 column:
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pCMY-SPORT6;
Site_2: Sall; Cloned unidirectionally. Proceedings and the process of the proc
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/clone="IMAGE:3852448"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL
http://image.llnl.gov
                                                                                                                                                                                                   Plate: LLCM1876 row: m column:
                                                                                                                                                                                                                                                                           cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Consortium (Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human.
                                                                                                                                                                           quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           559
                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5421109"
/clone_lib="NIH_MGC_110"
/tissue_type="ductal carcinoma,
                                                                                                                                                 Location/Qualifiers
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                                                                                           180 uTyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysL 197
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                                                                                                                                                                         164 ProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLe 180
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               197 ysAlaLeuLysLeuLysThrGluLeu 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 yAspGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLysSerL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 ThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGl 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 TGCCATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCCTCT
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AAGCTCTCAAGTTGCTGAAGACTGAATTG
                                                                           CTATGCTTACGAACCTGCAGATACAGCTCTGTTGCTTGACAACATGAAGA
                                                                                                                                                     CCATCTCTGACAGTTAGAGCCGATATCACTGGAAGATATTCAAACCGTCT 485
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/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Search time (sec): 1915.830000
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gb_pr:AF088867
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gb_pr:BC015503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oct 8,
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Sequence 265 from Patent W09953040.
AX015056
                                                                                                                                                                                                                                                                                                                                                                                                   Human nucleic acid sequences from ovarian tumour tissue Patent: WO 9953040-A 265 21-OCT-1999; SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE)
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                                                                                                                  Direct Submission
Submitted (30-AUG-1998) Pathology and Lab.
200 SW 1st St., Rochester, MN 55905, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     Homo sapiens putative secreted AF088867 AF088867.1 GI:6652811
                                                                                                                                                                        2 (bases 1 to 956)
Zhang, J.S. and Smith, D.I.
                                                                                                                                                                                                                           1 (bases 1 to 956)
Zhang, J.S. and Smith,
                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                               human
                                                                                                                                                                                                                                                        Mammalia; Eutheria;
                                                                                                                                                                                                               homolog of XAG
                       /note="differentially expressed in tumors; similar
Xenopus cement gland-specific secreted protein"
/codon_start=1
/product="putative secreted
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                                                                     148. .675
                                                                             /organism="Homo sapiens"
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                                                                                                         1. .956
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Primates;
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             protein XAG"
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seq_documentation_block:
LOCUS AF038451
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US-09-674-266A-181 x AF088867
                DEFINITION
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                                                                                                                                              Quality: 195.00
Ratio: 1.000
Similarity: 100.000
                                                                                                          etLysLysAlaLeuLysLeuLeuLysThrGluLeu 206
                                                                                                                                                                                                                                                                hrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMetPhe 161
                                                                                                                                                                                                                                                                                                                      eGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrT 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                yTrpGlyAspGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrL 95
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                                                                  gb_pr:AF038451
             Homo sapiens secreted
 mRNA, complete cds.
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/translation="mekipvsap-livalsytlard)tvkpgakkdtkdsrpkldptl
Srgwgodoliwygotyebalyksktsnkplmiihhldecphsqalkkvpaenkeloklae
opvllnlyyettdkhlspdggyvprimfvdpsltvraditgrysnrlyayepadtall
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            homolog
            PRI 03-DEC-1998 nolog (hAG-2/R)
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MEDLINE
REFERENCE
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JOURNAL
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TITLE
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152
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alignment_block:
US-09-674-266A-181 x AF038451
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                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: AF038451 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                        13 ProHisProSerArgArgLeuThrGlnGlyArgTrpValArgLysSerAr
euSerTyrThrLeuAlaArgAspThrThrValLysProGlyAlaLysLys
                                                                                                                                                                                     gValAlaMetGluLysIleProValSerAlaPheLeuLeuLeuValAlaL 46
                                                                                  TCTCCTACACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAAAAG
                                                                                                                                                                                                                                                    CCGCATCCTAGCCGCCGACTCACACAAGGCAGGTGGGTGAGGAAATCCAG
                                                                                                                                                                  AGTTGCCATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (09-DEC-1997) Surgery, Stanford
Road, MSLS Building, Room P228, Stanford,
Location/Qualifiers
1. 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thompson,D.A. and Weigel,R.J. hAG-2, the human homologue of the Xenopus laevis cement gland XAG-2, is coexpressed with estrogen receptor in breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thompson, D.A
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AF038451.1 GI:3779225
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Mammalia; Eutheria; Primates;
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1.000
100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="secreted cement gland protein XAG-2 homolog" /protein_id="AAC82614.1" /db_xref="GI:379926" /db_xref="GI:3797926" /tb_nsid="MSK79226" /translation="MSK79226" /translation="MSK7925FLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTL SRGWGDQLIWTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAE QFVLLNLYYETTDKHLSPDGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to Homo sapiens protein hAG-2/C deposited under GenBank Accession Number AF007791, and to Xenopus laevis cement gland-specific proteins np77 and XAG-2 deposited under GenBank Accession Numbers U82110 and AF025474, respectively"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="hAG-2/R"
59. .586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="breast"
/note="isolated from estrogen receptor-positive breast
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/db_xref="taxon:9606"
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Identity:
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KEYWORDS
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LOCUS AF115926
BASE COUNT
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Submitted (21-DEC-1998) Laboratory of Medicine and
Clinic, 200 SW 1st Street, Rochester, MN 55905, USA
Location/Qualifiers
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Zhang, J.S. and Smith, D.I.
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KEYWORDS
SOURCE
                                                     ACCESSION
VERSION
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US-09-674-266A-181
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                                                                                                   seq_documentation_block:
LOCUS BC015503
                                                                                                                                   seq_name:
                                                                                        DEFINITION
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                                                 Homo sapiens, anterior gradient 2 (Xenepus MGC:9112 IMAGE:3852448, mRNA, complete cds. BC015503 BC015503.1 GI:15930124
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                   Homo sapiens
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REMARK
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AUTHORS
TITLE
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US-09-674-266A-181 x BC015503
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lAlaMetGluLysIleProValSerAlaPheLeuLeuLeuValAlaLeuS 47
                                                                                                                                                                               TGCCATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCCCTCT 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 20 Row: o Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6652811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Emäil: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
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Sequence 1331 from Patent WO0196388
AX341084
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                           Patent: WO 0196388-A 1331 20-DEC-2001; CORIXA CORPORATION (US)
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AUTHORS
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AX231601.1 GI:15592500
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1 (bases 1 to 543)

Boyd, R.S., Stamps, A.C., Terrett, J.A. and Tyson, K.L.

Bcmp-7 as marker for diagnosis of breast cancer Patent: WO 0163290-A 7 30-AUG-2001;

Oxford GlycoSciences (UK) Limited (GB)

Location/Qualifiers

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alignment_block:
US-09-674-266A-181 x AX231601
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ORIGIN
                                                  seq_documentation_block:
LOCUS AF007791
                                                                                             seq_name: gb_pr:AF007791
 ACCESSION
                                  DEFINITION
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Homo sapiens secreted cement gland protein
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/db_xref="GI:15592501"
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TITLE
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                                                                                                                                                                                                                                                                              29 ArgValAlaMetGluLysIleProValSerAlaPheLeuLeuLeuValAl
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sSerLysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGluC
                                      TGGGGTGACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hAG-2, the human homologue of the Xenopus laevis cement gland XAG-2, is coexpressed with estrogen receptor in breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thompson, D.A. and
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Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF007791.1 GI:3779196
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1 (bases 1 to 838)
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SRGWGDQLIWTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAE
QFVLLNLVYETTDKHLSPDGQYVPRIMFVDPSLTVRADITGRYSNRLVAYEPADTALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="hAG-2/C"
/note="similar to Homo sapiens protein hAG-2/R deposited in GenBank Accession Number AF038451, and to Xenopus is GenBank Accession Number np77 deposited in GenBank Accession Number U82110 and XAG-2 deposited in GenBank Accession Number AF025474"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDNMKKALKLLKTEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="secreted cement gland protein XAG-2 homolog"
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/db_xref="GI:3779197"
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/db_xref="taxon:9606"
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1.000
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/cell_type="adenocarcinoma"
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Ratio: 1.000
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AR177367
AR177367.1 GI:17919722
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Edwards, J.-B. Dumas Milne., Duclert, A.
Complementary DNAs
Patent: US 6312922-A 61 06-NOV-2001;
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AX341234
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Mammalia; Eutheria;
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129 GlnLysLeuAlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrTh 145
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                                                           ArgValAlaMetGluLysIleProValSerAlaPheLeuLeuLeuValAl
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                                                AGAGTTGCCATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGC
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CCTCTCCTACACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAAA
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KEYWORDS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 2200 from Patent WO0196388
AX341953
                                                                                                                                                                                                                                                        Jiang,Y., Harlocker,S.L. and Secrist,H. Compositions and methods for the therapy
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CORIXA C
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                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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CORPORATION (US)
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Sequence 40 from Patent W00078960.
AX067336
AX067336.1 GI:12544960
Quality:
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                                                                                                                                            cancer
                                                                                                                                                     Compositions and methods
                                                                                                                                                               Yuqiu, J. and Mitcham, J.L.
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-DB-W_Geneseq_032802 -QFWMT=fastap -SUFFIX=011pZn.rng
-GAPOP=4.500 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCLT=0.000
-LOOPEXT=0.000 -QGAPOP=4.500 -GGAPEXT=0.050 -XGAPOP=60.000
-YGAPOP=6.000 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP-60.000
-YGAPOT=60.000 -DELOP=6.000 -FGAPEXT=7.000 -START=1
-MATRIX=011g0 -TRANS-human40.cdi -LIST=45 -DOCALIGN=200
-THR_SCORE-quality -THR_MIN=1 -ALIGN=15 -MODE-LOCAL -OUTFMT=pfs
-NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09674266_@CGM1_1_0 -NCPU=6 -ICPU=3 -LONGLOG
-USCRE-US09674266_@CGM1_1_0 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
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                                                                This invention describes novel polypeptides and their encoding nucleic acids derived from human pancreatic tumor tissue which have cytostatic activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. AAZ52858-Z53014 represent expressed sequence tag (EST) fragments derived from a human pancreatic tumor cDNA library and which encode the proteins represented in AAY73814-Y74252.
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Human protein; secret
KW Human protein; secret
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KW chemokinetic; thromboc
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P-PSDB; AAW37872.
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                                                                                                                                                                                                                                                                                                                                                                   12 GlyProHisProSerArgArgLeuThrGlnGlyArgTrpValArgLySSe
                                                                              LysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGl
hrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMetPhe
                                                                                                                                      ysSerLysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGlu
                                                                                                                                                                        TTGGGGTGACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATA
                                                                                                                                                                                   YTrpGlyAspGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrL
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SAGAMI CHEM RI
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CTGACAAACACCTTTCTCCTGATGGCCAGTATGTCCCCAGGATTATGTTT 462

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02-JUN-1999;
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The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1182, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1055, PRO1091, PRO2097, PRO1107, PRO1111, PRO11710, PRO2094, PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The PRO polypeptides and nucleotides are useful in the treatment, diagnosis and prevention of cancer. The antibodies and other anti-tumour compounds maybe used to treat various conditions, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; epithelial disorder;
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proliferation;
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Watanabe CK,
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bB; AAB24070.
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99US-0143048.
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99WO-US28313.
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                                                                                                                                                hrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMetPhe
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               nArgLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnM
                                                                  GTTGACCCATCTCTGACAGTTAGAGCCGATATCACTGGAAGATATTCAAA
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XX AAH35026;
XX O3-SEP-2001 (first 6
XX Human colon cancer ar
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KW Human; colon cancer;
KW Human; colon cancer;
KW Human; colon cancer;
XX Colorectal carcinoma;
XX Homo sapiens.
XX Homo sapiens.
XX PPN W0200122920-A2.
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XX W0200122920-A2.
XX W0200122920-A2.
XX W03-NOV-1999; 99US-(
XX PPSDB; ABG75621.
XX WFI; 2001-235357/24.
PF Ruben SM, Barash SC,
PF Ruben SM, Barash SC,
XX WFI; 2001-235357/24.
PF Nucleic acids encoding useful for preventing
XX W1; 2001-235357/24.
DR P-PSDB; AAG75621.
XX W1; 2001-235357/24.
DR P-PSDB; AAG75621.
XX W1; 2001-235357/24.
DR P-PSDB; AAG75621.
XX Claim 1; Page 3593; S
XX AAH32943 to AAH37195
CC cancer antigens have therapy and vaccine procedure associated with decreacy cancer antigens have therapy and treatment of cold associated with decreacy and treatment of cold                                                              alignment_block:
US-09-674-266A-181 x AAH35026
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Percent Similarity:
Align seg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders in a patient's genome that affect the activity of P by expressing in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated P, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB7789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                              N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 3593; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-235357/24.
P-PSDB; AAG75621.
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AAZ77486 standard; cDNA;
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                        09-APR-1998;
                                                                           21-OCT-1999
                                                                                                                            Homo sapiens.
                                                                                                                                                       gene
                                                                                                                                                                  Expressed sequence tag; EST; human; ovarian tumor; anticancer;
                                                                                                                                                                                            Human ovarian tumor cDNA library derived EST
                                                                                                                                                                                                                                                 AAZ77486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276 CCAAGACAAGCAACAAACCCTTGATGATTATTCATCACTTGGATGAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 GACACAAAGGACTCTCGACCCAAACTGCCCCAGACCCTCTCCAGAGGTTG
                                                09-APR-1998;
                                                                                                     DE19817557-A1
                                                                                                                                                                                                                      10-APR-2000
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                                                                                                                                                     therapy;
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                                                                                                                                                       treatment;
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METAGEN GES

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alignment_block:
US-09-674-266A-181 x AAZ77486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AAZ77486
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    129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the invention and encode the protein fragments represented in AAY76505-Y76638.
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Ratio: 1.000
Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProHisProSerArgArgLeuThrGlnGlyArgTrpValArgLysSerAr
nLysLeuAlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrThrA 146
                                                                         ProHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGl 129
                                                                                                                                            CCAAGACAAGCAACCCTTGATGATTATTCATCACTTGGATGAGTGC
                                                                                                                                                                  erLysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGluCys 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTTGCCATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCC
                                              CCACAGAGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAATAAAGAAATCCA
                                                                                                                                                                                                                                       GGGTGACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAAAT
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seq_documentation_block:
ID AAV19155 standard;
seq_name:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441
                                                                              New isolated human XAG growth factor(s) - used to for treating e.g. liver, lung or breast diseases hyperproliferative disorders, e.g. cancer.
                                                                                                                                                                                                                                                sig_peptide
                                                                                                                                                                                                                                                                                                      emphysema;
                                                                                                                                                                                                                                                                                                                                  Human XAG growth factor huXAG-1 cDNA
                                                                Claim 5; Fig 1; 141pp; English.
                                                                                                                    WPI; 1998-169093/15
                                                                                                                                                                               22-AUG-1997;
                                                                                                                                                                                                                                                                                                                     HuxAG-1; xAG;
                                                                                                            P-PSDB; AAW37844.
                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                23-AUG-1996;
                                                                                                                                                                                              26-FEB-1998
                                                                                                                                                                                                             WO9807749-A1
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                                                                                                                                                                                                                                                                                                             tumour marker;
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                                                                                                                                                                                                                                                                                                                                                                                                                    AGAAAGCTCTCAAGTTGCTGAAGACTGAATTG
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                                                                                                                                                                                                                                                                                                           growth factor; colon cancer-specific gene;
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71..130
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131..595
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This cDNA clone codes for huxAG-1 (see AAM37844), a member of a novel family of human growth factors also including huxAG-2 (see AAM37845) and huxAG-3 (see AAM37845). These proteins share homology with the xAG protein of Xenopus laevis, which is involved in embryogenesis and is expressed in adult tissue. Expression of huxAG-1 has been discovered in colon cancer tissue, with no corresponding expression in healthy colon tissue. The huxAG-1 gene, also designated colon cancer-specific gene (CCSG), provides a molecular marker for

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alignment_block:
US-09-674-266A-181 x AAV19155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibodies, and screening methods for identifying agonists and antagonists of huxAG-1 are provided. HuxAG polypeptides are growth factors and can be used to stimulate proliferation of cells. They can be used to stimulate the proliferation and differentiation of hepatocytes to alleviate or treat liver diseases and pathologies such as fulminant liver failure caused by cirrhosis, liver damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  colon cancer. huXAG-1 cDNA was isolated from a cDNA library derived from human colon cancer tissue. Vectors, host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  particular hepatocellular carcinoma, osteoclastoma, breast cancer. or colon cancer. The products can also be used for detection and
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                                                           GGCAGAGCAGTTTGTCCTCCTCAATCTGGTTTATGAAACAACTGACAAAC
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0 other

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seq_documentation_block:
ID AAF63314 standard; cf
XX AAF63314;
XY O4-MAY-2001 (first 6
XX Human huXAG-1/CCSG cc
XX Human huXAG-1/CCSG cc
XX Human huXAG-1/CCSG cc
XX Homo sapiens.
XX Homo sapiens.
XX US6171816-B1.
XX US6171816-B1.
XX 22-AUG-1997; 97US-1
XX 23-AUG-1996; 96US-1
XX 23-AUG-1996; 96US-1
XX PD 09-JAN-2001.
XX PD 09-JAN-2001.
XX PD 09-JAN-2001.
XX PP 22-AUG-1997; 97US-1
XX PP 22-AUG-1997; 97US-1
XX PP 22-AUG-1997; 97US-1
XX HOMA-) HUMAN GENOME
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XX P-PSDB; AAB72203.
XX P-PSDB; AAB72203.
XX Novel human growth f
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PT the lungs and for id
XX Novel human growth f
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PT the lungs and for id
XX Claim 45; Fig 1; 59p
XX This invention relat
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                                                                                                                                               This invention relates to a human growth factor polypeptide huXAG-1 also CC known as a colon cancer specific gene (CCSG). HuXAG-1 stimulates cell CC proliferation as a growth factor. The HuXAG-1 protein is useful for cidentifying compounds capable of enhancing or inhibiting cellular response induced by huXAG-1. The protein is also useful for stimulating CC proliferation of cells e.g. colon, breast, liver and lung cells, and the pathologies such as fulminant liver failure caused by cirrhosis, liver CC damage caused by viral hepatitis and toxic substances, for preventing and CC treating damage to the lungs caused by various pathological states and CC cancer. HuXAG-1 and the identified antagonist are useful for treating cancer in particular colon cancer between the gene encoding huXAG-1 is useful for monitoring human colon cancer. States and the identified antagonist are useful so fhuXAG-1 cancer in particular colon cancer for diagnosing or detecting cancer in changes cancer in the gene encoding huXAG-1 is useful for monitoring human colon cancer. HuXAG-1 carcinoma. huXAG-1 is useful for monitoring human colon cancer in the first polynuclectides are useful for diagnosing or detecting cancer in the first polynuclectides are useful for monitoring human colon cancer. HuXAG-1 carcinoma. huXAG-1 is useful for monitoring human colon cancer.
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seq_documentation_block:
ID AAV59320 standard; cl
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AC AAV59320;
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DT 21-DEC-1998 (first e
XX
DE Nucleotide sequence e
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KW bacterial colonisatio
KW chronic obstructive p
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ss; human; mucous-mediated function; adhesion; tumour metastasis; bacterial colonisation; microbial infection; AIDS; cystic fibrosis; chronic obstructive pulmonary disease; asthma; Crohn's disease;
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Ratio: 1.000
Similarity: 100.000
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                                                                                                                                                                                                                                         rAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysA 198
                                                                                                                                                                                                                                                                                          SerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeuTy 181
                                                                                                                                                                                                                                                                                                                                        isLeuSerProAspGlyGlnTyrValProArgIleMetPheValAspPro 164
                                                                                                                                                                                                                                                                                                                                                                                       uAlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrThrAspLysH 148
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                                                                                                                                                                                                                                TGCTTACGAACCTGCAGATACAGCTCTGTTGCTTGACAACATGAAGAAAG
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                                                                                                                                                         /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV59320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The human polypeptide zsigl0 is involved in mucous-mediated functions such as adhesion. The products of the invention can be used in the study and treatment of e.g. tumour metastasis, bacterial colonisation, susceptibility to and persistence of infection, microbial infections, AIDS, cystic fibrosis, chronic obstructive pulmonary disease, asthma, sinonasal inflammatory disease, inflammatory bowel disease, bronchitis, or Crohn's disease. The products can also be used for detection, diagnosis and drug screening.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated mucous-associated polypeptide, zsig10 - used to develop products for treating e.g. tumour metastasis, microbial infections, cystic fibrosis, asthma, bronchitis or inflammatory bowel disease
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P-PSDB; AAW77365.
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erAsnLysProLeuMetIleIleHisHisLeuAspGluCysProHisSer
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Breast cancer cell me
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                Diagnosing, preventing and treating breast cancer using a breast cancer cell membrane protein BCMP 7\, -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes the novel use of a protein found in breast cancer cell membranes (BCMP 7) for diagnosing, preventing and treating breast cancers. The peptide has cytostatic action and potential uses in gene therapy and in vaccines. The polypeptide, antisense nucleic acids, or fusion proteins comprising and Green Fluorescent protein or the DsRed Fluorescent protein, antibodies specific for and/or nucleic acid are used for the prevention and/or treatment of breast cancer. Antibodies against may also be used for screening for and/or diagnosis of breast cancer in a patient. The method for monitoring/assessing breast cancer treatment in a patient and for the identification of metastatic breast cancer cells in samples from a patient. This sequence encodes breast cancer cells associated protein 7 (BCMP 7), located on chromosome 7p21.3, described in the method of the invention.
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US-09-674-266A-181
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13-APR-1998;
10-AUG-1998;
                                                                                                                                                                         soluble proteins. The sequences can be used for chromosome mapping and identification of genes associated with hereditary diseases or drug response. Signal sequences from the cDNAs can be used in construction of secretion vectors. Other sequences derived from the extended cDNAs can be used to clone upstream genomic DNA sequences including promoters. This is in turn useful for identifying proteins that interact with promoter sequences. Some of the proteins may be useful in diagnosing and treating several disorders including, but not limited to: cancer, hyperlipidaemia, cardiovascular and neurodegenerative disorders, autoimmune diseases, and rheumatic diseases, embryogenic disorders, hypertension, renal injury, amino acidurias, hypoglycaemia, male rat infertility and myopathies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome mapping; human; hereditary disease; diagnosis; cancer; hyperlipidaemia; cardiovascular; neurodegenerative disorder; therapy; autoimmune disease; rheumatic disease; embryogenic disorder; myopathy; renal injury; amino aciduria; hypoglycaemia; male rat infertility; hypertension; ss.
                                                                                                                                                                                                                                                                                                                                                         This sequence encodes a human secreted protein of the invention. The extended cDNAs (or genomic DNAs obtainable from them) may be used to prepare PCR primers and probes. These are useful for forensic matching or positive identification by DNA sequencing. They may also be used in alternative fingerprint identification techniques. Antibodies against the proteins encoded by the extended cDNAs are useful in identification of tissue types or cell species, as well as identifying tissue specific
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P-PSDB; AAY59675.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142
                                                                                                                                   Human protein; secretory signal; nutritional source; immunity; haematopoiesis; activin; inhibin; tumour; chemokinetic; thrombolytic; anti-inflammatory; inhibi
                                                                                                                                                                                                                                                                                                                                          492
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                                                                                                                                                                                                                                                                                                                                                                                            162 alaspProSerLeuThrValargAlaaspIleThrGlyArgTyrSerAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342 CAGAAATTGGCAGAGCAGTTTGTCCTCCTCAATCTGGTTTATGAAACAAC
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                                                                                                                           stomach
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                                                                                                                                                                                                                        AAV29048;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 AGAGTTGCCATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGC
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                                                                                                                                                                                                                                                                                                            tLysLysAlaLeuLysLeuLeuLysThrGluLeu 206
                                                                                                                                                                                                                                                                                                                                         AGGACACAAAGGACTCTCGACCCAAACTGCCCCAGACCCTCTCCAGAGGT
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                                                                                                                                                                                                                                                                                                TTGACCCATCTCTGACAGTTAGAGCCGATATCACTGGAAGATATTCAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                            TGACAAACACCTTTCTCCTGATGGCCAGTATGTCCCCCAGGATTATGTTTG
                                                                                                      sapiens
                                                                                                                                                                              reading
                                                                                                                                                                                                                                                                          /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:AAV29048
                                                                                                                           cancer
                                                                                                                                                                               frame
                                                                                                                                                                                                   (first entry)
                                                                                                                           cell;
                                          /product=
                                                                      Location/Qualifiers
1..525
                                                                                                                                                                              human
                                                                                                                                                                                                                                             cDNA;
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                                                                                                                                                                                                                                             525
                                                                                                                                                                              protein comprising secretory signal
                                   signal"
                                                 "human
                                                                                                                                                                                                                                             ВP
                                                  comprising
                                                                                                                                      inhibition;
                                                  secretory
                                                                                                                                                          cytokine;
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19-MAR-1998

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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the nucleotide sequence of the open reading frame of a novel human protein comprising a secretory signal (AAV29047), isolated from stomach cancer cells. Its proteins can be used as nutritional sources or supplements. The proteins may also have cytokine functions, immune modulating functions, haematopoiesis regulating activity, activinyinhibin regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity.
                                                                                                132
                                                                                                                                                                115
                                                                301
                                                                                                                                251
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                                                                                                                                                                                                                                                                                                                             101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 525 BP; 162 A; 131 C; 103 G; 129 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Pages 88; 131pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human proteins with secretory signal sequences - used to tree immune deficiencies, infections, tumours, and haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-207380/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders, etc.
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                                                                               AlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrThrAspLysHi 148
                                                                                                                                                 erGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGlnLysLeu 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MetGluLysIleProValSerAlaPheLeuLeuLeuValAlaLeuSerTy
               GTCAAGCTTTAAAGAAAGTGTTTGCTGAAAATAAAGAAATCCAGAAATTG
                                                                                                                                                                                              AAGCAACAAACCCTTGATGATTATTCATCACTTGGATGAGTGCCCACACA
                                                                                                                                                                                                               rSerAsnLysProLeuMetIleIleHisHisLeuAspGluCysProHisS 115
                                                                                                                                                                                                                                                             CAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAAATCCAAGAC
                                                                                                                                                                                                                                                                              GlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLysSerLysTh
                                                                                                                                                                                                                                                                                                                           AGGACTCTCGACCCAAACTGCCCCAGACCCTCTCCAGAGGTTGGGGTGAC
                                                                                                                                                                                                                                                                                                                                              ysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGlyAsp
                                                                                                                                                                                                                                                                                                                                                                                          CACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAAAAGGACACAA
                                                                                                                                                                                                                                                                                                                                                                                                            rThrLeuAlaArgAspThrThrValLysProGlyAlaLysLysAspThrL
                                                                GCAGAGCAGTTTGTCCTCCTCAATCTGGTTTATGAAACAACTGACAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGCCCCTCTCCTA
Quality:
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seq_documentation_block:
ID AACOUll5 standard; cD
XX AACOUll5;
XX AACOUll5;
XX Human secreted proteil
XX Human; 5' EST; expres
KW Human; 5' EST; cy
RP 1033401-A2.
XX 20-FEB-1999; 99US-0
XX 21-FEB-2000; 2000EP-0
XX 26-FEB-1999; 99US-0
XX AGEST ) GENSET.
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XX The present sequence
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                                                                                  alignment_scores:
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                                                                                                                                                                                                                                                 The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID 113; 71pp + CD-ROM; English
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                        Quality:
Ratio:
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                                                                                                                                                                           142 A;
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Gaps:
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Percent Similarity:

Percent Identity: 100.000

Align seg 1/1

to: AAC00115

from: 1

to: 468

US-09-674-266A-181 x AAC00115

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seq_documentation_block:
ID AAF44884 standard;
                                                                                                                                                                                                                                                                                                                                                          seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAF44884
                                                                                                                                                                                                                                                        Human breast cancer related protein coding sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                  413
                                                                                                                                                                                                                                                                                                                                                                                                        145
                                                                                                                                                                                                                                                                                                                                                                                                                              363
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       \ensuremath{\mathsf{New}} polynucleotides encoding breast tumor specific proteins, useful prevention, treatment and diagnosis of breast cancer -
                                                                                                           23-JUN-1999;
12-OCT-1999;
                                                                                                                                          23-JUN-2000; 2000WO-US17536
                                                                                                                                                                                       WO200078960-A2
                                                                                                                                                                                                                                   Human; breast
                                                                                                                                                                                                                                                                                28-MAR-2001
                                                                                                                                                                 28-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   laLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAlaLys
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                                                                                                                                                                                                                                                                                                                                                                                             hrAspLysHisLeuSerProAspGlyGlnTyrValPro 157
                                                                                                                                                                                                                                                                                                                                                                                                                              CCAGAAATTGGCAGAGCAGTTTGTCCTCCTCAATCTGGTTTATGAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                          eGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCTCTCCTACACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAA
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                                                                                                                                                                                                                                                                                                                                                                                  CTGACAAACACCTTTCTCCTGATGGCCAGTATGTCCCA 450
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                                          2001-041426/05.
                                                             'n
                                                                Mitcham JL;
                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                  cancer; diagnosis; therapy; vaccine;
                                                                                                         99US-0140903
99US-0158980
                                                                                                                                                                                                                                                                                                                            cDNA;
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seq_documentation_block:
ID AAA77903 standard; cD
XX
AC AAA77903;
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PM 14-NOV-2000 (first e
DE CDNA encoding human c
XX
KW Human colon tumour po
KW immunotherapy; diagno
XX
OS Homo sapiens.
XX
PN W0200037643-A2.
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Quality: 134.00
Ratio: 1.000
Percent Similarity: 100.000
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US-09-674-266A-181 x AAF44884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides the coding sequences for a number of breast cancer related proteins. These can be used in vaccinations against, diagnosis of and treatment of cancer, particularly breast
                                                                                                                                                                                                                                                                                                                   425
                                                                                                                                                                                                                                                                                                                                                                                                                    325
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                                                                                                                                                                                                                                                                               170 aAspIleThrGlyArgTyrSerAsnArgLeuTyrAlaTyrGluProAlaA 187
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                                                Human colon tumour polypeptide; tumour
immunotherapy; diagnosis; progression;
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                                                                                                                                                                                                                                                                                                                                                                             euLeuAsnLeuValTyrGluThrThrAspLysHisLeuSerProAspGly 153
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                                                                                                                                                                                                                                                                                                                                                                    TCCTCAATCTGGTTTATGAAACAACTGACAAACACCTTTCTCCTGATGGC
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                                                                                                                                                           cDNA;
                                                                                     colon tumour polypeptide,
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Gaps:
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                                                  antigen;
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                                                                                     SEQ ID NO:183
                                                              cancer;
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                                                                vaccine;
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alignment_block:
US-09-674-266A-181 x AAA77903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences AAA77722-A78199 represent 478 cDNAs encoding proteins or corritors of proteins which are associated with human colon tumours. The invention also specifically discloses 8 human colon tumour proteins (CABB11897-B11904). The nucleic acids, the polypeptides they encode, and antigen presenting cells (APCs, preferably dendritic cells) expressing cells untigen presenting cells (APCs, preferably dendritic cells) expressing cells presently colon tumour cells, thereby inhibiting the development of cancer. T-cells specific for the polypeptide expressed by the APC are cells and to remove tumour cells from biological samples, especially blood or cractions thereof. The sample or the isolated T-cells specific for the collypeptide can then be used to inhibit cancer development. CD4+ and/or cells T-cells from a patient may be incubated with a polypeptide or closed and then administered back to the patient to inhibit cancer cells are proliferation of specific T-cells. The T-cells can be cause the proliferation of specific T-cells. The T-cells can be captained and then administered back to the patient to inhibit cancer cells are prospected back to the patient to inhibit cancer cells are prospected encoding the polypeptides and antibodies against the polypeptides may be used to determine the expression level concer cells are present. Such diagnostic methods may also be used to cancer cells are progression of a cancer by repeating the processes at time colline to the processes at time colline to the processes at time colline to the processes at time colline the processes at time colline to the process
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02-JUL-1999;
22-SEP-1999;
19-NOV-1999;
02-DEC-1999;
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                                                                                                           rLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGlyA 81
                                                                                                                                                                                                TyrThrLeuAlaArgAspThrThrValLysProGlyAlaLysLysAspTh
                    spGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLysSerLys
                                                                                                                                                                         TACACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAAAAGGACAC
                                                                                    AAAGGACTCTCGACCCAAACTGCCCCAGACCCTCTCCAGAGGTTGGGGTG
ACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAAATCCAAG
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, Yuqiu J;
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                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
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99US-0347496.
99US-0401064.
99US-0444242.
99US-0454150.
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Benson DR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 T; 0 other;
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160
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAI28641
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                                                                                                                                                                                                                                                                                                                                  30-DEC-1999;
10-JAN-2000;
15-FEB-2000;
06-MAR-2000;
19-MAY-2000;
29-JUN-2000;
The present invention describes colon tumour associated proteins (I) and the polynucleotides (II) that encode them. (I) have cytostatic activity. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immunotherapy; diagnosis; colon cancer; colon tumour;
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                                                                                                                                                             Claim 25; Page 184; 472pp; English.
                                                                                                                                                                                       prevention,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lmmunogenic; gene therapy; vaccine;
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3E, Wang T,
                                                                                                                                                                                                                                                                                                                    2000US-0480321.
2000US-0504629.
2000US-0519444.
2000US-0575251.
2000US-0609448.
2000US-0649811.
                                                                                                                                                                                       associated proteins and nucleic acids useful for diagnosis and treatment of colonic cancer - \,
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                                                                                                                                                                                                                                                                      Stolk
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cell culturing the cell to express the protein. (II) and its complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (PCR) and hybridisation assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (I) may also be used as antigens in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. Anti-(I) antibodies and antagonists may also be used to down regulate TCAP expression and activity. The anti-(I) antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AAI28460 to AAI29512 and AAM24494 to AAM24523 represent nucleotide and amino acid sequences given in the exemplification of the present invention.

9999999999998×8

Sequence 409 BP; 131 A; 104 C; 80 G; 94 T; 0 other;

alignment_scores:
Quality: 133.00 Length: 133
Quality: 13000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-674-266A-181 x AAI28641 ...

Align seg 1/1 to: AAI28641 from: 1 to: 409

131261148311164

HisLeuSerProAspGlyGlnTyrValProArgIleMetPheValAspPr 164

360

euAlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrThrAspLys 147

TGGCAGAGCAGTTTGTCCTCCTCAATCTGGTTTATGAAACAACTGACAAA 310

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9b_est2:BI523582

9b_est2:BG179160

9b_est2:BE748141

9b_est2:BM129777

9b_est1:AW956284
                                          gb_est2:BG259927
gb_est2:BF747277
gb_est2:BF513917
gb_est1:AA316233
gb_est1:AA316233
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Database length: -1841457050
Search time (sec): 1725.590000
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gb_est2:BG610804
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gb_est1:AW582256
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Query: US-09-674-266A-181
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                                                                                                                                                                                                                           gb_est1:AA437001
gb_est1:AA314372
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gb_est2:BI770077
gb_est1:AL543472
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gb_est2:BM006510
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gb_est2:BG386151
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gb_est2:BE870718
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-TRANKS=human40 cd1 -LIST-45 -DOCALIGN-200 -THR_SCORE=quality
-THR_MIN=1 -ALIGN-15 -MODE-LOCAL -OUTFW1=pfs -NORM-ext
-HARPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09674266_@CGN1_1_2564 -NCPU-6 -ICPU-3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
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-Q-/cgn2_1/USPF0_spool/US99674266/runat_08102002_093408_26991/app_query.fasta_1.271
-DB-EST -OFMT-fastap -SUFFIX-olippn.rst -GAPOP-4.500
-GAPEXT=0.050 -MINANTCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000
-QGAPOP-4.500 -QGAPEXT=0.050 -XGAPOP-60.000 -XGAPEXT-60.000
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-60.000 -YGAPEXT-60.000
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.5e-129
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.3e-127
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.0e-164
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.8e-160
.1e-152
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.2e-175
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BE748141 601571509F1 NIH_MGC_55
BM129777 1523a08.y1 Melton Norm
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700 QV3-DT0012-291299-051-
77 60237188991 NHL,MGC 93
77 RC1-BT0254-271100-121-
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EST187946 HCC cell li
EST039 Human hepatoce
EST187482 Colon carci
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gb_est1:AA315116
gb_est1:AA315166
gb_est1:AW166169
gb_est2:BG501149
gb_est2:BF680021
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Location/Qualifiers
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Tissue Procurement: DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
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/db_xref="taxon:9666"
/clone="IMAGE:4806679"
/clone="IMAGE:4806679"
/clone=lib="NIH_MGC_00"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/lab_host="digragectuggcc); Site_2: Sit! (ggccattatggcc); Site_1: Sit! (ggccattatggcc); Site_2: Si
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s cDNA clone IMAGE:4806679 5',
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ACCESSION
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AUTHORS
TITLE
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ORGANISM
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LOCUS AW582256
                                                                                                                                                                                    COMMENT
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2=QV4-ST0212-
120100-075-e10&t3=2000-01-12&t4=1)
                                                                                                                                                                                                HCGP http://www.ludwig.org.br/ORESTES
The FAPESP/LICR Human Cancer Genome Pu
Unpublished (1999)
                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 689)
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                                                                                 Tel: +55-11-2704922
Fax: +55-11-2707001
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/clone_lib="ST0212"
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46 euSerTyrThrLeuAlaArgAspThrThrValLysProGlyAlaLysLys
                                                                              29 gValAlaMetGluLysIleProValSerAlaPheLeuLeuLeuValAlaL 46
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Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Plate: LLAM11504 row: h column: 04
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                        190
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-*Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: ECORV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MCC Library.*
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/clone_lib="NIH_MGC_122"
/]ab boc+-"profer
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/db_xref="taxon:9606"
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/clone="IMAGE:4431583"
/clone_lib="NIH_MGC_91"
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102 TCTCCTACACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 ProHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGl 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 gLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          452 GACCCATCTCTGACAGTTAGAGCCGATATCACTGGAAGATATTCAAATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 CCACACAGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAATAAAGAAATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 GGGTGACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAAAT 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 CCAAGACAAGCAACAAACCCTTGATGATTATTCATCACTTGGATGAGTGC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 erLysThrSerAsnLysProLeuMetIleTleHisHisLeuAspGluCys 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pGlyAspGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLysS
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                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10186 row: o column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BULLYLLU 750 bp mRNA linear EST 06-FEB-2001 602330032F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4431583 5',
                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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                                                                                    quality sequence stop:
                                            1. .750
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                               Location/Qualifiers
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US-09-674-266A-181 x BG179160
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Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 hrSerAsnLysProLeuMetIleIleHisHisLeuAspGluCysProHis 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGlnLysLe 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLysSerLysT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yrThrLeuAlaArgAspThrThrValLysProGlyAlaLysLysAspThr 64
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                                                                                                                                                                                                                                                                                                                                              LysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGlyAs 81
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                                                                                                                          laLeuLysLeuLeuLysThrGlu 205
                                                                                                                                                                                                     rAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysA 198
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/lab_host="NHIOB (phage:resistant)"
/note="Organ: prostate; vector: pcMv-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NH_MGC Library."

174 c 158 g 183 t 1 others
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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                       31 aMetGluLysIleProValSerAlaPheLeuLeuLeuValAlaLeuSerT 48
AAGGACTCTCGACCCAAACTGCCCCAGACCCTCTCCAGAGGTTGGGGTGA
                           LysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGlyAs 81
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Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: CLONETECH Laboratories, I cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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Location/Qualifiers
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/db_xref="taxon:9666"
/clone="IMAGE:383847"
/clone="IMAGE:383847"
/tissue_type="from acute myelogenous leukemia"
/tissue_type="from acute myelog
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COMMENT
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                                                                                                          Fax: 617-495 0007, Email: dmelton@biohp.harvard.edu
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing
Library was constructed by Dr. Douglas Melton DNA sequencing
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Other_ESTs: if23a08.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave MA 02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hiller,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.
                                                                                                                                                                                                                     Tel: 617-495-1812
Fax: 617-495-8557
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                  ValArgAlaAspIleThrGlyArgTyrSerAsnArgLeuTyrAlaTyrGl 184
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/dev_stage="Adult"
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/sex="Both"
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Contact: John Quackenbush
Contest: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 3528
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 721) Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Hol., L., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST368354 MAGE resequences, MAGD Homo sapiens cDNA, mRNA sequence. AW956284
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM795 row: d column: 17
High quality sequence stop: 748.
Location/Qualifiers
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Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
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/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
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/clone="IMAGE:3942112"
/clone_lib="NIH_MCC_7"
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Ratio: 1.000
Percent Similarity: 100.000
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Align seg 1/1 to: BE870718 from: 1 to: 734
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                                                                         ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLe 137
                                                                                                                                                                                    etileileHisHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120
                                                                                                                                                                                                                                                                                                                                                                GACATATGAAGAAGCTCTATATAAATCCAAGACAAGCAACAAACCCTTGA 251
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uLeuAsnLeuValTyrGluThrThrAspLysHisLeuSerProAspGlyG
                                                                                                                                                        TGATTATTCATCACTTGGATGAGTGCCCACACAGTCAAGCTTTAAAGAAA 301
                                                      GTGTTTGCTGAAAATAAAGAAATCCAGAAATTGGCAGAGCAGTTTGTCCT
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="adenocarcinoma"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo d'average insert size 1.8 kb. Library constructed by LiTechnologies. "
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BG285246.1 GI:13037011
EST.
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Tissue Procurement: DCTD/DTP
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10467 row: i column: 18
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian
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/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: Not Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

194 c 189 g 212 t 1 others
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                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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183 rGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysAlaLeuL
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections (1988)
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CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (CDNA Sequencing by: NIH Intramural Sequencing Center Clone distribution: MGC clone distribution informations of the control of
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ysProHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIle 128
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/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
30 a 181 c 153 g 187 t
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Ratio: 1.000
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62 ysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGly
                                                                                                                          81
                                                                                                                                                                                                  45 aLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAlaLysL
                                                                                                                                                                                                                                                                         31 AGAGTTGCCATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGC
                                                                                                                                                                                                                                                                                                                                                    29 ArgValAlaMetGluLysIleProValSerAlaPheLeuLeuLeuValAl
                                                                                                                  CCTCTCCTACACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAAA
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 758)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/site_2: EcoRI; cDNA made by oligo-dT priming.
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/site_3: CDNA mad
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                                                                                                                                                                         cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM1877 row: 1 column: 16 High quality sequence stop: 792. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian
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Mammalia; Eutheria; Primates;
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/organism="Homo sapiens"
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/note="Organ: pancreas; Vector: poTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
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BM006784.1 GI:16521138
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603615217F1 NIH_MGC_110 Homo
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Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                          162 alaspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsn 178
                                                                                                                                                                                                                                                                                                                                                                                                                112 ysProHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIle 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 TGGGGTGACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 AGGACACAAAGGACTCTCGACCCAAACTGCCCCAGACCCTCTCCAGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGACAAACACCTTTCTCCTGATGGCCAGTATGTCCCCCAGGATTATGTTTG
                                                        tLysLysAlaLeuLysLeuLysThrGluLeu 206
                                                                                                               CGTCTCTATGCTTACGAACCTGCAGATACAGCTCTGTTGCTTGACAACAT
                                                                                                                              ArgLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMe
                                                                                                                                                                                  TTGACCCATCTCTGACAGTTAGAGCCGATATCACTGGAAGATATTCAAAC
                                                                                                                                                                                                                                                                       rAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMetPheV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sSerLysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGluC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGly
                                       GAAGAAAGCTCTCAAGTTGCTGAAGACTGAATTG
                                                                                                                                                                                                                                                                                                                                                                                                   GCCCACACAGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAATAAAGAAATC
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gb_est2:BM006784
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129 GlnLysLeuAlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrTh 145
                                                                                                                                                          95 sSerLysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGluC
                                                                                                                                                                                                                                                                                                                                              62 ysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGly 78
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                                                                                                                                                                                                                                                                                                                      GCCCACACAGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAATAAAGAAATC
                                                                       ysProHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIle 128
                                                                                                                                         ATCCAAGACAAGCAACAAACCCTTGATGATTATTCATCACTTGGATGAGT 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGAGTTGCCATGGAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Robert St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 802)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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http://image.llnl.gov
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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/tissue_type="ductal carcinoma, cell line"
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Site_2: EcoRI; cDNA made by oligo-dT priming.
Site_2: EcoRI; cDNA made by oligo-dT priming the following 5' adaptor: GGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_est2:BM006554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
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http://image.llnl.gov
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178.00
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alignment_block:

Ratio: Percent Similarity:

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Percent Identity:

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Align seg 1/1 to: BM006554
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                                                                                  TrpGlyAspGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLy
      tLysLysAlaLeuLysLeuLeuLysThrGluLeu 206
                           ArgLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMe 195
GAAGAAAGCTCTCAAGTTGCTGAAGACTGAATTG
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Database: Issued_Patents_NA:*
Database sequences: 383533
Database length: 122816752
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-Q=/cgn2_1/USPTO_spool/USO9674266/runat_08102002_093409_27017/app_query.fasta_1.271
-DB=-Issued_Patents_Na -QPMT=fastap_ -SUFFIX=011p2n.rni
-GAPOP=4.500 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000
-XGAPEXT=60.000 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000
-YGAPEXT=60.000 -DELDCP=6.000 -DELEXT=7.000 -YGAPOP=60.000
-YGAPEXT=60.000 -DELDCP=6.000 -DELEXT=7.000 -YGAPOP=60.000
-TRANS-human40.cdi -LIST=45 -DOCALIGN=20
-THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE-LOCAL -OUTFWT=pfs
-NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-USO9674266_@CGNI_1.46 -NCDU=6 -ICDU=3 -LONGLOG
-DEV TIMFOUTE=100 -MANDAN THEORY - ALIGN=1 - ALIGN=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-123-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /ptodata/1/ina/6B_COMB.seq:US-09-247-155-149 + 
/ptodata/1/ina/6B_COMB.seq:US-08-916-576B-36 +
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102.00 1150.01
14.00 974.26
52.00 974.26
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53.00 985.36
38.00 700.35
24.00 432.00
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2.2e-16
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2.9e-47
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489
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alignment_block:
US-09-674-266A-181
                                                                                                                                    alignment_scores:
                                                                   Percent Similarity:
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Patent No.
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NAME/KEY:
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                                                                                                               Quality:
                                                                                           Ratio:
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WARN:

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; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-916-576B-1
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-030-607-160-
/cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-39-313-160-
/cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-794-002-5-
/cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-854-039B-5-
/cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-854-039B-1-
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                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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STATE: DC
COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                    STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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131..595
                     sig_peptide
71..130
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US-08-916-576B-1

192.00 1.000 100.000

Percent

Gaps: : Identity:

192 0 100.000

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APPLICANT: Dumas Milne Edwards, Jean-Baptiste APPLICANT: Duclert, Aymeric APPLICANT: Bougueleret, Lydie TITLE OF INVENTION: Complementary DNAS FILE REFERENCE: GENSET.021A CURRENT APPLICATION NUMBER: US/09/247,155A CURRENT EILING DATE: 1999-02-09 EARLIER APPLICATION NUMBER: 60/074,121 EARLIER APPLICATION NUMBER: 60/081,563 EARLIER APPLICATION NUMBER: 60/081,563 EARLIER FILING DATE: 1998-04-13 EARLIER FILING DATE: 1998-04-13 EARLIER APPLICATION NUMBER: 60/096,116 EARLIER APPLICATION NUMBER: 60/096,116 EARLIER APPLICATION NUMBER: 60/099,273 EARLIER FILING DATE: 1998-00-04 EARLIER FILING DATE: 1998-10-04 NUMBER: 60/099,273 EARLIER FILING DATE: 1998-10-04
                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-247-155-61
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; NAME/KEY: polyA_site
; LOCATION: 1674..1689
US-09-247-155-61
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US-09-674-266A-181 x US-09-247-155-61
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LOCATION: 51..575
EEATURE:
NAME/KEY: $19_peptide
LOCATION: 51..110
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 11.2
OTHER INFORMATION: seq AFLLLVALSYTLA/RD
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 1653..1658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo
FEATURE:
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                                                                                           TTGACCCATCTCTGACAGTTAGAGCCGATATCACTGGAAGATATTCAAAT
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Gaps: 0
Percent Identity: 100.000
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Ratio: 1.000
Percent Similarity: 100.000
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APPLICATION NUMBER: US 60/024,347

FILING DATE: 23 AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: STEEFE, ERIC K.

REGISTRATION NUMBER: 36,688

REGISTRATION NUMBER: 1488.0500001

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (202) 371-254 INFORMATION FOR SEQ ID NO:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 386 base pairs
115 erGlnAlaLeuLysLysValPheAlaGluAsnLysGluILeGlnLysLeu 131
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                                                                            98 rSerAsnLysProLeuMetIleIleHisHisLeuAspGluCysProHisS 115
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                                                                                                                                    CAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAAATCCAAGAC 113
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EBNER, REINHARD
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alignment_block:
US-09-674-266A-181 x US-09-040-984-78
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                                                                                                                                                         Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Reed, Steven G.
APPLICANT: Wang, TongTong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
TITLE OF INVENTION: OF LUNG CANCER
NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 18-MAR-19
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LENGTH: 793 base pairs
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STATE:
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                                                                                                                                                                                                                                                                                            LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 206-282-603:
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Percent Identity:
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seq_documentation_block:
Sequence 78, Application US/09123912A
Patent No. 6312695
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
FILE REFERENCE: 210121.455C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-123-912-78
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Pa
SEQ ID NO 78
LENGTH: 793
                                                                                       LOCATION: (563)
OTHER INFORMATION: Where n
NAME/KEY: modified_base
LOCATION: (657)
OTHER INFORMATION: Where n
NAME/KEY: modified_base
LOCATION: (660)
OTHER INFORMATION: Where n
NAME/KEY: modified_base
LOCATION: (703)
OTHER INFORMATION: Where n
NAME/KEY: modified_base
LOCATION: (708)
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OTHER INFORMATION: where n NAME/KEY: modified_base LOCATION: (711)
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LOCATION: (309)
OTHER INFORMATION: Where n
NAME/KEY: modified_base
LOCATION: (492)
OTHER INFORMATION: Where n
NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/123,912A CURRENT FILING DATE: 1998-07-27 PRIOR APPLICATION NUMBER: 09/040,802 PRIOR FILING DATE: 1998-03-18 NUMBER OF SEQ ID NOS: 114
                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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; OTHER INFORMATION: Where US-09-123-912-78
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US-09-674-266A-181 x US-09-123-912-78
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Quality:
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                                                                   Sequence 32, Application US/09221298 Patent No. 6284241 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
           APPLICANT: Xu. Jiangchun
TITLE OF INVENTION: COMPOUNDS AND METHODS
TITLE OF INVENTION: OF COLON CANCER
FILE REFERENCE: 210121.471
CURRENT APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: where NAME/KEY: modified_base LOCATION: (787)
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OTHER INFORMATION: Where
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                                                                                                                                                                                                                                                                                                                                                                                              CCTACACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAAAAGGAC
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                                           DIAGNOSIS
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FILE REFERENCE: GENSET.021A
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,116
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US-09-674-266A-181 x US-09-221-298-32
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; ORGANISM: Human
US-09-221-298-32
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; Sequence 149, Applicat
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Quality:
                                                                                                                            : NUMBER OF SEQ ID NOS: 182
: SOFTWARE: Patent.pm
: SEQ ID NO 149
: SEQ ID NO 149
: LENCTH: 940
: TYPE: DNA
: ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-247-155-149
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NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence 149, Application US/09247155A Patent No. 6312922 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dumas Milne Edwards, Jean-Baptiste APPLICANT: Duclert, Aymeric APPLICANT: Bougueleret, Lydie TITLE OF INVENTION: Complementary DNAs
                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: 60/099,273 EARLIER FILING DATE: 1998-10-04
                                                                                                              FEATURE:
                                                                 NAME/KEY: CDS
LOCATION: 177..569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 401
NAME/KEY: sig_peptide LOCATION: 177..236
                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 PheValAspProSerLeuThrValArgAla.AspIleThrGlyArgTyrS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 hrThrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMet 160
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98.750
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0:
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alignment_block: us-09-674-266a-181 \times us-09-247-155-149
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; LOCATION: 482
; OTHER INFORMATION: n=a,
US-09-247-155-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-916-576B-36
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6171816
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                          ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 11.1999998092651
OTHER INFORMATION: seq AFLLLVALSYTLA/RD
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             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: STERNE, K
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318
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                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 AGAGTTGCCATGGAAAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTGGC
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                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600 CITY: WASHINGTON
                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                   STATE:
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6171816
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VENTION: NOVEL HUMAN GROWTH FACTORS
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alignment_block:
US-09-674-266A-181 x US-08-916-576B-36
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Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 209, Application US/09030607 Patent No. 6262245
                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 1: MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 CTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAAAAGGACACAAAG
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STATE: WA
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                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                    USA
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  (206) 622-4900
06) 682-6031
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Percent Identity: 100.000
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                                                                                                                                                                                                                   Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LENGTH: 159 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-030-607-209
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Quality:
alignment_block:
                                                                                              alignment_scores:
                                                                                                                                                         ; ORGANISM: Homo sapien US-09-439-313-209
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                                        Percent Similarity:
                                                                                                                                                                                         APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 209
LENGTH: 159
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-09-030-607-209
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 209,
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, Jiangchun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 CTCTCC
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                                                                        Quality:
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                                                        Ratio:
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Retter, Mark
Solk, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reed, Steven G.
Kalos, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jiang Yuqui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harlocker, Susan Louise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dillon, Davin C.
Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158
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                                      : 52.00
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                                      Gaps: 0
Percent Identity: 100.000
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alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                        US-08-916-576B-37
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  Ratio:
Percent Similarity:
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APPLICANT: YU, GUO
APPLICANT: DILLON,
APPLICANT: ESNER,
APPLICANT: ENDRESS
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                                                                                                                                  LENGTH: 158 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                       TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                          NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 141
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
CORRESPONDENCE STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION UDATA:

APPLICATION NUMBER: US 60/024,347

FILING DATE: 23-AUG-1996

ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
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STATE: DC
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DILLON, PATRICK J.
EBNER, REINHARD
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Percent Identity:
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                                       Length:
                  Gaps:
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seq_documentation_block:
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US-09-674-266A-181 x US-08-916-576B-37
US-08-916-576B-9
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APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK
APPLICANT: EBNER, REINHARD
                                                                                                                                                                                                                                                  TELEFAX: (202) 371-254
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                          TOPOLOGY: 1
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
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                                                                                                                         STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                  LENGTH:
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alignment_scores:

Quality:

38.00 1.000 100.000

Percent Identity:

Length:

: 38 : 0 : 100.000

Ratio: Percent Similarity:

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alignment_block:
US-09-674-266A-181 x US-08-916-576B-10
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US-09-674-266A-181 x US-08-916-576B-9
                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-916-576B-10
                                                                                                                                                                                  US-08-916-576B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-916-576B-9 from: 1
                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/08916576B Patent No. 6171816
                                                                                                                                                                                                                                                                                                                  TELEFAX: (202) 371-25. INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/024,347 FILING DATE: 23-AUG-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 506 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140
                                                                                                                                                                                                  TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 aLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAlaLysL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 ysAspThrLysAsp 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90
                                                                                                                                                                                                                                                                                                                                                                                            NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1100 NEW CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/916,576B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGACACAAAGGAC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTCTCCTACACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAAA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20005-3934
                                                                                                                                                                                                                                                        nucleic acid
                                                                                Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
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                                                                                                                                                                                                                                                                                                                                      (202) 371-2540
                                                                                                                                                                                                                      linear
                                                              1.000
                                                                                                                                                                                                                                    single
                                                                                                      37.00
                                                                                                                                                                                                                                                                                                                                                        371-2600
                                                              Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                            1488.0500001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version #1.30
                                                                                                    Length:
                                                                                Gaps:
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alignment_block:
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                                     US-09-674-266A-181 x US-08-916-576B-38
 Align seg 1/1
                                                                                              Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 371-25.
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,347
FILLING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                            TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 136 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                 NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0500001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 TAAAGAAATCCAGAAATTGGCAGAGCAGTTTGTCCTCCTCAATCTGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 nLysGluIleGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeuValT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 LeuAspGluCysProHisSerGlnAlaLeuLysLysValPheAlaGluAs 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 TTGGATGAGTGCCCACACAGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1100 NEW CITY: WASHINGTON STATE: DC
                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                     LENGTH: 130 DEL
TENGTH: 130 DEL
TYPE: nucleic acid
sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38,
                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8, Application US/08916576B 6171816
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                                                                                                              Ratio:
to: US-08-916-576B-38 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: US-08-916-576B-10 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                    (202) 371-2600
                                                                                          33.00
1.000
100.000
                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                              371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOVEL HUMAN GROWTH FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/916,576B
                                                                                            Gaps:
Percent Identity:
 to: 136
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                                                                                              100.000
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alignment_scores:
Quality:
Ratio:
Percent Similarity: 1
alignment_block:
US-09-674-266A-181 x US-08-916-576B-5
                                                                                                                                              ; NAME/KEY:
; LOCATION:
US-08-916-576B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-916-576B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08916576B Patent No. 6171816
                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/08/916 FT.LING DATE:

CLASSITEM: US/08/916 FT.

CLASSITEM: US/08/916 FT.
                                                                                                                                                                                                         FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,347
FILLING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 140
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29
                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: WASHINGTON
                                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                    732 base pairs
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49.:546
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118..546
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49..117
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                                                 Percent Identity:
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Gaps:
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